

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:43:41 ; Search time 50 Seconds  
(without alignments)  
661.732 Million cell updates/sec

Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDDRMKOHMDERAPI.....IYEQDADSKHGTYWYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA: \*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pdp: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pdp: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pdp: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pdp: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCRTUS COMB.pdp: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pdp: \*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pdp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1821	87.3	384	1	US-08-872-302-4 Sequence 4, Appli
2	1510	72.4	374	2	US-09-059-769-4 Sequence 4, Appli
3	1493	71.6	374	2	US-09-059-769-2 Sequence 2, Appli
4	1427.5	68.4	375	2	US-09-161-994A-2 Sequence 2, Appli
5	1279	61.3	383	2	US-09-638-937-15 Sequence 15, Appl
6	1271	60.9	383	2	US-09-059-769-12 Sequence 12, Appl
7	1271	60.9	383	2	US-09-161-994A-16 Sequence 16, Appl
8	1234	59.2	383	2	US-09-059-769-11 Sequence 11, Appl
9	1234	59.2	383	2	US-09-161-994A-15 Sequence 15, Appl
10	1234	59.2	383	2	US-09-837-751-31 Sequence 31, Appl
11	1226	58.8	383	2	US-09-837-751-6 Sequence 6, Appli
12	1224.5	58.7	382	1	US-08-872-302-2 Sequence 2, Appli
13	1215	58.2	383	1	US-08-314-596-41 Sequence 41, Appl
14	1215	58.2	383	1	US-08-320-982-41 Sequence 41, Appl
15	1215	58.2	383	2	US-08-819-037-41 Sequence 41, Appl
16	1215	58.2	383	2	US-08-530-862B-6 Sequence 6, Appli
17	1215	58.2	383	2	US-08-597-313D-6 Sequence 6, Appli
18	1215	58.2	383	2	US-09-059-769-9 Sequence 9, Appli
19	1215	58.2	383	2	US-09-161-994A-14 Sequence 14, Appl
20	1215	58.2	383	2	US-09-133-962A-2 Sequence 2, Appli
21	1215	58.2	383	2	US-09-045-940-41 Sequence 41, Appl
22	1215	58.2	383	2	US-09-763-331-4 Sequence 4, Appli
23	1215	58.2	383	2	US-09-697-379-2 Sequence 2, Appli
24	1215	58.2	383	2	US-10-116-212A-2 Sequence 2, Appli
25	1215	58.2	383	2	US-09-885-189-6 Sequence 6, Appli
26	1215	58.2	383	2	US-09-837-751-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-08-872-302-4  
; Sequence 4, Application US/08872302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,302  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Majarian, William R  
; REGISTRATION NUMBER: P-41,173  
; REFERENCE/DOCKET NUMBER: BB-1084  
; TELEPHONE: 302-992-4926  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-302-4

Query Match 87.3%; Score 1821; DB 1; Length 384;  
Best Local Similarity 84.3%; Pred. No. 1.6e-179;  
Matches 322; Conservative 29; Mismatches 27; Indels 4; Gaps 1;  
QY 1 MSDSYDDR---MKDHMDERAPIDPAPPSLDLKAIPAHCPRSAVSSCVVQDLII 56  
Db 3 MSDSCDDHQLVKDHNINERAPVDAAPPSLDLKAIPAHCPRSAVSSCVVQDLII 62  
QY 57 TFLTYTANTYIPLPLPLVLAWPVYWFQCSCILTLGLVWLGHECGHHAFFSEYQWIDNAV 116

Db 63 TELLYTLANSIPLPPPLPYLAWPVYWFQSSILTLGLWIGHECHHAYSEYQVNDTV 122  
QY 117 GFVLHSALLTPYFWMKYSHRKHANTNSLENEEVIPRTQSLRTYSTYFELDNTPPGRIL 176  
Db 123 GFILHSPLLTYPYFWMKYSHRKHANTNSLENEEVIPKAKSLRNYSNPKFLDNTPGRI 182  
QY 177 ILVIMLTGPPLYLTLNUSGKYDRFTNHFDPDLSPIFTRERIRIQVALSDGLGIVAVFYGLK 236  
Db 183 ILLIMLTGFLYLLTLNIGSKYQYRPFANHFDPDLSPIFTRERIRIQVLSDVGLIIVFYGLK 242  
QY 237 FLVOTKFGWVMCMYGVPIVGLNSFIITVYLLHHTLSSPHYDSTEWNIKALTTIDRD 296  
Db 243 FLVAKGFGWVMYGVAPVGLNFIITVYLLHHTLSSPHYDSTEWNIKALTTIDRD 302  
QY 297 FGLNRVFDVTHVHLHLPYIPIHYHAKASEAIKPILDGYRMDRTPFFKAMWREAK 356  
Db 303 FGLNRVFDVTHVHLHLPYIPIHYHAKASEAIKPILDGYRMDRTPFFKAMWREAK 362  
QY 357 ECIYIEQDADSKHKGTYYHYKM 378  
Db 363 ECIYIEPDEDKKHGYYHYKM 384

## RESULT 2

US-09-059-769-4  
; Sequence 4, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-059-769-4  
Query Match 72.4%; Score 1510; DB 2; Length 374;  
Best Local Similarity 70.4%; Pred. No. 2.1e-147;  
Matches 261; Conservative 50; Mismatches 56; Indels 4; Gaps 2;  
QY 8 RMKDHDMDERAPIDPAPFSLDLKKAIPAHCFRBSAVWSSCYVVQDIIITELLTYVANTY 67  
Db 8 RTSEKVMERSVSDPVTFLSLDLKQAIPPHCFQRSSVIRSSYYVQDIIIAVIFYELANTY 67  
QY 68 IPHLPPLPYLAWPVYWFQSSILTLGLWIGHECHHAFSEYQVNDNAVGFLHSALLTP 127  
Db 68 IPNLPHPLAYLAWPLYWFCQASVLTGLWILGHECHHAYSNTYVDDTVGFIHSLJLTP 127  
QY 128 YFSWKYSHRKHANTNSLENEEVIPRTQSLRTYSTYFELDNTPPGRILILVIMLTGPP 187  
Db 128 YFSWKYSHRKHANTNSLENEEVIPRTQSLRTYSTYFELDNTPPGRILILVIMLTGPP 185  
QY 188 LYLTLNUSGKYDRFTNHFDPDLSPIFTRERIRIQVALSDGLGIVAVFYGLKFLVOTKFGW 247  
Db 186 LYLTLNUSGKYDRFTNHFDPDLSPIFTRERIRIQVALSDGLGIVAVFYGLKFLVOTKFGW 245  
QY 248 MCMYGVPIVGLNSFIITVYLLHHTLSSPHYDSTEWNIKALTTIDRDGLNVEHVDV 307  
Db 246 ACMYGVPIVGLNSFIITVYLLHHTLSSPHYDSTEWNIKALTTIDRDGLNVEHVDV 305  
QY 308 THTVHLHLPYIPIHYHAKASEAIKPILDGYRMDRTPFFKAMWREAKECIYIEQDADS 367  
Db 306 THTVHLHLPYIPIHYHAKASEAIKPILDGYRMDRTPFFKAMWREAKECIYIEQDADS 363  
QY 368 KHGTYHYHYKM 378  
Db 364 KLKGYYHYHYKM 374  
RESULT 3  
US-09-059-769-2  
; Sequence 2, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706



Db 79 HPLSVAMPLVFCOGSVLTGVWVIAHCGHAFSDYQWLDDTVGLLHLSALLVYFPMK 138  
QY 133 YSHRKHANTNSLENEVYIPRTQSOLRTYSTYFELDNTPGRILILVIMLTGLFPLYLTL 192  
Db 139 YSHRHHNTGSLERDEVFVPKRGISWSS--EVLNPPGRVLVLLVQLTLGWPPLYLMF 196  
QY 193 NVSGKKYDRFTNHPDPLSPIETERERIQVALSDLGIVAFVGLKFLVOTKPGWVMCMVG 252  
Db 197 NVSGRPDRFACHFPKSPINDRERLQIYISDAGIVAMVGLYRLVAAKGVAVWVCYIG 256  
QY 253 VPVIGLNSFIIVITVYLHHTLSSPHYSTENWIKGALTITDTRDFGLNLRVFDVTHV 312  
Db 257 VLLVNGFLVILTYLQHTQPSLPHYDSSEWDLKALATVDYDYGFLNKVLNITDTHV 316  
QY 313 LHLFPYIPHYHAKESBAIKPILGDYRMDRTPPFKAMWEAKECIYIEQADSKHGT 372  
Db 317 AHLFPSTPHYHAMEATKAIPKILGDYQCDRTVPFKAMYREKVECIYVEADGDNKGV 376  
QY 373 YWY 375  
Db 377 FWY 379

## RESULT 6

US-09-059-769-12  
; Sequence 12, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxysenase Genes and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GreenLee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 383 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Solanum commersonii  
US-09-059-769-12  
Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 1.1e-122;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;  
QY 16 ERAPIDPAPFSLDLKKAIPAHCFERSAVWSSCYVVDLIITFLTYTANTYIPLHPPPL 75  
Db 22 QKVPTSKPFTVGDIIKKAIPHCQFORSIRFSYVYVDLILVSIYVANTYFHLPSY 81  
QY 76 VYLAMPVYVFCOSCLITGLWVLGHCCHAFSEYQWIDNAVGVFLHLSALLTPYFQWKYSH 135  
Db 82 CVIAWPIYVICQGCVCCTGIWVNAHCGHAFSDYQWDDTVGLILHLSALLVYFQWKYSH 141  
QY 136 RKHHANTNSLENEVYIPRTQSOLRTYSTYFELDNTPGRILILVIMLTGLFPLYLTLNVS 195  
Db 142 RRHSNTGSLERDEVFVPKPKSQLGWSKY--LNNPPGRVLSLTITLTGLWPLYLAFNVS 199  
QY 196 GKKYDRFTNHPDPLSPIETERERIQVALSDLGIVAFVGLKFLVOTKPGWVMCMVGVPV 255  
Db 200 GRPYDRFACHYDPYGPYNNRERLQIFISDAGVLGVCYLLYRIALVKGLAMLVCYGVPL 259  
QY 256 IGLNSFIIVITVYLHHTLSSPHYSTENWIKGALTITDTRDFGLNLRVFDVTHVHLH 315  
Db 260 LVNGLFLVILTYLQHTQPSLPHYDSTEWDLRGALATCDRDYGVNLKVFNHITDTHVVHH 319  
QY 316 LFPYIPHYHAKESBAIKPILGDYRMDRTPPFKAMWEAKECIYIEQADSKHGTWY 375  
Db 320 LFSTMPHYNAMEATKAIPKILGDYQCDRTVPFKAMYREKVECLYVEADGSGGVFWY 379  
RESULT 7  
US-09-161-994A-16  
; Sequence 16, Application US/09161994A  
; Patent No. 6333448  
; GENERAL INFORMATION:  
; APPLICANT: BAFOR, Maureen  
; APPLICANT: BANAS, Antoni  
; APPLICANT: DAHLQVIST, Anders  
; APPLICANT: GUMMESON, Per-Olov  
; APPLICANT: LEE, Michael  
; APPLICANT: SJODAL, Staffan  
; APPLICANT: STYMNE, Sten  
; APPLICANT: LENMAN, Marit  
; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF  
; FILE REFERENCE: BAFOR-1  
; CURRENT APPLICATION NUMBER: US/09/161,994A  
; CURRENT FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 9601236.4  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-161-994A-16  
Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 1.1e-122;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;  
QY 16 ERAPIDPAPFSLDLKKAIPAHCFERSAVWSSCYVVDLIITFLTYTANTYIPLHPPPL 75  
Db 22 QKVPTSKPFTVGDIIKKAIPHCQFORSIRFSYVYVDLILVSIYVANTYFHLPSY 81  
QY 76 VYLAMPVYVFCOSCLITGLWVLGHCCHAFSEYQWIDNAVGVFLHLSALLTPYFQWKYSH 135



Db 82 CYTANPIYWCQCVCCTGIWNAHECGHAFSDYQWVDDTVGLILHLSALLVPYFWSKYSH 141  
Qy 136 RKHANTNSLENEBEVYIPRTQSQLRTYSTYEFDLNTPGRILILVIMLTGLGFPLYLNTVS 195  
Db 142 RRHSNTSGSLERDEVFVKPKSQLGWSKY--LNNPPGRVLSTLTTLGWPLYLAFNVS 199  
Qy 196 GKXDRFTWHFDPLSFIFTERERIQVALSDLGIVAVPYGLKFLVQTKGFGWVCMYGVV 255  
Db 200 GRPYDRFACHYDPGYPIYNNRRLQIFISDAGVLGVCYLLRYALVKGLAWLCVYGVPL 259  
Qy 256 IGLNSFIIVITYLHHTHLSGPHYDSTENWNIKGALTIDRDFGLLNVRVHDVTHVLHH 315  
Db 260 LVVNGFLVITYLQHTSPHSDSTENWNLGALATCDRDYGLNKNVFNHITDTHVHH 319  
Qy 316 LPFYIPHYHAKASEAIKPIGLDYRMDRTFFPKAMWREAKECIYIEQADSKHGTYWY 375  
Db 320 LFTSTMPHYNAMEATKAVKPLGDDYQFDGTPYIKENWREAKECLYVEKDESSQKGWFY 379

RESULT 8  
US-09-059-769-11  
; Sequence 11, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Styume, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 383 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:

; ORGANISM: Glycine max  
US-09-059-769-11  
Query Match 59.2%; Score 1234; DB 2; Length 383;  
Best Local Similarity 57.0%; Pred. No. 7.2e-119;  
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;  
Qy 7 DRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRRSAMVSSCYVVOODLIITFLLYTVANT 66  
Db 13 NRKSEVDPLKRVPFEPKQFSLQIKKAIPHCQFQSVLRSFSYVVDLTIAFCLYVATH 72  
Qy 67 YIPLHPPPLVYLAWPVYFQCSCILTLGLVHGECGHAFSEYQWIDNAGVFLHLSALLT 126  
Db 73 YFHLPGPLSFGMALIYAVQGCILTGWVWIAHECGHAFSDYQLDDDIIVGLILHLSALLV 132  
Qy 127 PYFSWKYSHRKHANTNSLENEBEVYIPRTQSQLRTYSTYEFDLNTPGRILILVIMLTGLF 186  
Db 133 PYFSWKYSHRHSNTSGSLERDEVFVKPKSQLGWSKY--LNNPPGRVLSTLTTLGW 190  
Qy 187 PLYLLTNVSGKYDRFTNHFDPISPIPTERERIQVALSDLGIVAVPYGLKFLVQTKGFGW 246  
Db 191 PLYLALNVSGRPYDRPACHYDPGYPIYSDRERLQIYISDAGVLAVVYGLFRLAMAKGLAW 250  
Qy 247 VMCYGVGPVIGLNSFIIVITYLHHTHLSGPHYDSTENWNIKGALTIDRDFGLLNVRVHD 306  
Db 251 VVCYGVGPLLVNGFLVITYLQHTHPALPHYTSEWDLRGALATVDRDYGLNKNVFNH 310  
Qy 307 VTHTHVLHLLFPYIPHYHAKASEAIKPIGLDYRMDRTFFPKAMWREAKECIYIEQAD 366  
Db 311 IDTTHVAHLFSTMPHYNAMEATKAIKPIGLGEYRDETFPVKAMWREARECIYVEPDQS 370  
Qy 367 SKHGTYWYH 376  
Db 371 TESKGVFWYN 380

RESULT 9  
US-09-161-994A-15  
; Sequence 15, Application US/09161994A  
; Patent No. 6333448  
; GENERAL INFORMATION:  
; APPLICANT: EAPOR, Maureen  
; APPLICANT: BANAS, Antoni  
; APPLICANT: DAHLQVIST, Anders  
; APPLICANT: GUMMESON, Per-Olov  
; APPLICANT: LEE, Michael  
; APPLICANT: STODAL, Staffan  
; APPLICANT: STYNN, Sten  
; APPLICANT: LENMAN, Marit  
; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF  
; FILE REFERENCE: BAFOR=1  
; CURRENT APPLICATION NUMBER: US/09/161,994A  
; CURRENT FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 9601236.4  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-161-994A-15  
Query Match 59.2%; Score 1234; DB 2; Length 383;  
Best Local Similarity 57.0%; Pred. No. 7.2e-119;  
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;  
Qy 7 DRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRRSAMVSSCYVVOODLIITFLLYTVANT 66  
Db 13 NRKSEVDPLKRVPFEPKQFSLQIKKAIPHCQFQSVLRSFSYVVDLTIAFCLYVATH 72  
Qy 67 YIPLHPPPLVYLAWPVYFQCSCILTLGLVHGECGHAFSEYQWIDNAGVFLHLSALLT 126

Db 73 YFLLPGPLSPRGMAIYWAQCCILITGVWVIAHECGHAFSDYQLDDDIVGLILHSALLV 132  
Qy 127 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 186  
Db 133 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 190  
Qy 187 PLYLLTNVSGKKYDRFTNHFDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFGW 246  
Db 191 PLYLLTNVSGKKYDRFTNHFDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFGW 250  
Qy 247 VMCWYGVPIGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHD 306  
Db 251 VCVYGVPLLVNGFLVLTITFLOHTHPALPHYTSSEWDLRGALATVDRDYGILNKVFN 310  
Qy 307 VTHTVLHLLPPIPHYHAKSEAIKPIGLGYRMDRTTFFKAMWREAKECIYEQDAD 366  
Db 311 ITDTHVAHLFSTMPHYHAMEATKAIPILGEYRFDETPFVKAMWREARECIYVEPDQS 370  
Qy 367 SKHKGTYWYH 376  
Db 371 TESKGVFWYN 380

RESULT 10  
US-09-837-751-31  
; Sequence 31, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-837-751-31

Query Match 59.2%; Score 1234; DB 2; Length 383;  
Best Local Similarity 57.0%; Pred. No. 7.2e-119;  
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;  
Qy 7 DRMKDHDDERADIPAPPSLSDLKKAIPACFRSRAVWSSCYVQDLITITLLTYVANT 66  
Db 13 NRKSEVDPLKRVFPFKPQPSLQIKAIPACFRSRAVWSSCYVQDLITITLLTYVANT 72  
Qy 67 YFLLPGPLSPRGMAIYWAQCCILITGVWVIAHECGHAFSDYQLDDDIVGLILHSALLV 126  
Db 73 YFLLPGPLSPRGMAIYWAQCCILITGVWVIAHECGHAFSDYQLDDDIVGLILHSALLV 132  
Qy 127 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 186  
Db 133 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 190  
Qy 187 PLYLLTNVSGKKYDRFTNHFDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFGW 246  
Db 191 PLYLLTNVSGKKYDRFTNHFDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFGW 250  
Qy 247 VMCWYGVPIGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHD 306  
Db 251 VCVYGVPLLVNGFLVLTITFLOHTHPALPHYTSSEWDLRGALATVDRDYGILNKVFN 310  
Qy 307 VTHTVLHLLPPIPHYHAKSEAIKPIGLGYRMDRTTFFKAMWREAKECIYEQDAD 366  
Db 311 ITDTHVAHLFSTMPHYHAMEATKAIPILGEYRFDETPFVKAMWREARECIYVEPDQS 370

Qy 367 SKHKGTYWYH 376  
Db 371 TESKGVFWYN 380  
RESULT 11  
US-09-837-751-6  
; Sequence 6, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Gossypium sp.  
US-09-837-751-6

Query Match 58.8%; Score 1226; DB 2; Length 383;  
Best Local Similarity 56.9%; Pred. No. 4.8e-118;  
Matches 205; Conservative 72; Mismatches 81; Indels 2; Gaps 1;  
Qy 16 ERAPIDPAPPSLSDLKKAIPACFRSRAVWSSCYVQDLITITLLTYVANTYIPHLPPPL 75  
Db 22 KRVYSKPPFTLSEIKKAIPACFRSRAVWSSCYVQDLITITLLTYVANTYIPHLPPPL 81  
Qy 76 VYLAWPVYWFQSCILITGLWVLGHECHHAFSEYQWIDNAVGVFLHSAITLTPYFSWKYSH 135  
Db 82 SNVAPLYWAMQGCILITGVWVIAHECGHAFSDYQLDDDIVGLILHSALLVYFSPWKYSH 141  
Qy 136 RKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPIYLLTNVS 195  
Db 142 RRHSNTGSLERDEVFPVKKSGLRWAKH--FNNPPGRFLSITITLGLMPLYLAFNVA 199  
Qy 196 GKDYDRFTNHFDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFWWCMYGVVP 255  
Db 200 GRPYDRFACHYDPGPIFSDRERLQIYISDAGVLAVALYRLVLAKGVGVISYGVPL 259  
Qy 256 IGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHDVTHVHLH 315  
Db 260 LVVNAFLVMTIYLTQHTHPSLPHYDSSEWDMRGALSTVDRDYGILNKVFNITDTHVAH 319  
Qy 316 LPYIPHYHAKSEAIKPIGLGYRMDRTTFFKAMWREAKECIYEQDADSKHKGTYWY 375  
Db 320 LFTMPHYHAMVATKAIPILGEYQFDGMPVPYKAIMWEAKECLYVEPDGDKGVFWF 379

RESULT 12  
US-08-872-302-2  
; Sequence 2, Application US/088722302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:



/ COUNTRY: U.S.A.  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/320,982  
/ FILING DATE: 11-OCT-1994  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/314,596  
/ FILING DATE: 26-SEP-1994  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: KOKULIS, PAUL N.  
/ REGISTRATION NUMBER: 16,773  
/ REFERENCE/DOCKET NUMBER: 206905/1220  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-861-3000  
/ TELEFAX: 202-822-0944  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 383 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-08-320-982-41

Query Match 58.2%; Score 1215; DB 1; Length 383;  
Best Local Similarity 55.6%; Pred. No. 6.6e-117; Indels 2; Gaps 1;  
Matches 205; Conservative 70; Mismatches 92;

QY	8	RMKDMDERAPIDPAPFSLDLKKAIPAHCPFRSAVMSVQVQDLIITFLTYVANTY	67
Db	14	KKSETDTTKRVCEKPPFSGDLKKAIPHCPKRSIPRPSFSLISDIIIIASCFFYVATNY	73
QY	68	IPHLPPPLVYLAWPVYVFCQSCILTGLWLHCEGHAFSEYQWIDNAVGVFLHSLTTP	127
Db	74	FSLLPQPLSYLAWPLYWACQGCVLGTIWIHAECHGHAFSDYQWLDDTVGLIFHSFLVLP	133
QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRTYSTVEFLDNTPGRILLIIVMLTLGFP	187
Db	134	YFSWKYSHRRHSNTGSLERDEVFPVKOKSAIKWYGY--LNNPLGRIMMLTVQVFLGWP	191
QY	188	LYLLTNVSGKYDRFTNHPDPLSPFITERERIQVALSDLGIVAVFYGLKFLVQTGFGWV	247
Db	192	LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGMASM	251
QY	248	MCYGVVPVIGLNSFIIVITYLHHTLSPPHYDSTENWIKGALTTIDRDPGLLNRFVHDV	307
Db	252	ICLYGVPLLI VNAFLVITYLQHTHPSLPHYDSSEWDLRGALATVDRDYGLNKVFHNI	311
QY	308	THTHVLHLFPYIPHYHAKASEATKPLGDYRMDTRTPPFKAMWREAKECIYISODADS	367
Db	312	TDTHVAHLFSTMPHYNAMEATKAIPILGDYQFDGTPWYVAMVREAKECIYVSPDREG	371
QY	368	KHKGYTWYH 376	
Db	372	DKKGYTWN 380	

RESULT 15  
US-08-819-037-41  
/ Sequence 41, Application US/08819037  
/ Patent No. 6028248  
/ GENERAL INFORMATION:  
/ APPLICANT: SOMERVILLE, CHRIS  
/ APPLICANT: VAN DE LOO, FRANK  
/ TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
/ TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
/ NUMBER OF SEQUENCES: 48

/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.  
/ STREET: 1100 NEW YORK AVENUE, N.W.  
/ CITY: WASHINGTON  
/ STATE: D.C.  
/ COUNTRY: U.S.A.  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Microsoft Word  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/819,037  
/ FILING DATE: 19-MAR-1997  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/320,982  
/ FILING DATE: 11-OCT-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/314,596  
/ FILING DATE: 26-SEP-1994  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 383 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-08-819-037-41

Query Match 58.2%; Score 1215; DB 2; Length 383;  
Best Local Similarity 55.6%; Pred. No. 6.6e-117; Indels 2; Gaps 1;  
Matches 205; Conservative 70; Mismatches 92;

QY	8	RMKDMDERAPIDPAPFSLDLKKAIPAHCPFRSAVMSVQVQDLIITFLTYVANTY	67
Db	14	KKSETDTTKRVCEKPPFSGDLKKAIPHCPKRSIPRPSFSLISDIIIIASCFFYVATNY	73
QY	68	IPHLPPPLVYLAWPVYVFCQSCILTGLWLHCEGHAFSEYQWIDNAVGVFLHSLTTP	127
Db	74	FSLLPQPLSYLAWPLYWACQGCVLGTIWIHAECHGHAFSDYQWLDDTVGLIFHSFLVLP	133
QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRTYSTVEFLDNTPGRILLIIVMLTLGFP	187
Db	134	YFSWKYSHRRHSNTGSLERDEVFPVKOKSAIKWYGY--LNNPLGRIMMLTVQVFLGWP	191
QY	188	LYLLTNVSGKYDRFTNHPDPLSPFITERERIQVALSDLGIVAVFYGLKFLVQTGFGWV	247
Db	192	LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGMASM	251
QY	248	MCYGVVPVIGLNSFIIVITYLHHTLSPPHYDSTENWIKGALTTIDRDPGLLNRFVHDV	307
Db	252	ICLYGVPLLI VNAFLVITYLQHTHPSLPHYDSSEWDLRGALATVDRDYGLNKVFHNI	311
QY	308	THTHVLHLFPYIPHYHAKASEATKPLGDYRMDTRTPPFKAMWREAKECIYISODADS	367
Db	312	TDTHVAHLFSTMPHYNAMEATKAIPILGDYQFDGTPWYVAMVREAKECIYVSPDREG	371
QY	368	KHKGYTWYH 376	
Db	372	DKKGYTWN 380	

Search completed: September 22, 2006, 19:45:04  
Job time : 52 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	2086	100.0	378	9	ADM68587	Stokesia
2	2077	99.6	378	9	AEC02369	Stokesia
3	1821	87.3	384	2	AW83354	Vernonia
4	1549.5	74.3	377	8	ADR87355	Hydroxyyla
5	1549.5	74.3	377	8	ADR87357	Codon opt
6	1549.5	74.3	377	8	ADR87361	Codon opt
7	1549.5	74.3	377	9	AEC02271	Stokesia
8	1549.5	74.3	377	9	AEC02275	Stokesia
9	1549.5	74.3	377	9	AEC02289	Stokesia
10	1523.5	73.0	377	4	AAW70946	C. offici
11	1510	72.4	374	2	AAW79743	Crepis sp
12	1504	72.1	374	8	ADR87360	Codon opt
13	1504	72.1	374	9	AEC02274	Crepis bi
14	1499	71.9	374	9	AEC02370	Crepis bi
15	1498	71.8	374	8	ADR87337	Hydroxyyla
16	1498	71.8	374	9	AEC02251	Crepis bi
17	1497	71.8	374	9	AEC02368	Crepis pa
18	1493	71.6	374	2	AAW79742	Crepis pa
19	1493	71.6	374	8	ADR87450	Crepis pa
20	1482	71.0	380	8	ADR87343	FAD2/Hydr
21	1482	71.0	380	9	AEC02257	Crepis bi
22	1458	69.9	372	9	ADX69239	Delta-12
23	1458	69.9	372	9	ADX85618	C. palae

Query Match 100.0%; Score 2086; DB 9; Length 378;  
Best Local Similarity 100.0%; Pred. No. 1.3e-215;  
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60  
Db 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60

Qy 61 YTVANTYIPLPPLVYLWVPVYFCQSCILTLGLWVLCGHCCHAFSEYQWIDNAGFVL 120  
Db 61 YTVANTYIPLPPLVYLWVPVYFCQSCILTLGLWVLCGHCCHAFSEYQWIDNAGFVL 120

Qy 121 HSALLTPVFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYVEFLDTPGRILILVI 180  
Db 121 HSALLTPVFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYVEFLDTPGRILILVI 180

Qy 181 MTLGFPPLLYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVPYGLKFLVQ 240  
Db 181 MTLGFPPLLYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVPYGLKFLVQ 240

Qy 241 TKFGVWCMYGVVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300  
Db 241 TKFGVWCMYGVVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300

Qy 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPIIGDYRMIDRTPPFKAMWREAKECIY 360  
Db 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPIIGDYRMIDRTPPFKAMWREAKECIY 360

Qy 361 IEQDADSKHKGTYYWHKM 378  
Db 361 IEQDADSKHKGTYYWHKM 378

RESULT 2  
AEC02369  
ID AEC02369 standard; protein; 378 AA.  
AC AEC02369;  
DT 06-OCT-2005 (first entry)  
DE Stokesia laevis epoxigenase SEQ ID NO.136.  
KW transgenic plant; anhelmintic; epoxigenase.  
OS Stokesia laevis.  
XX US2005172358-A1.  
XX 04-AUG-2005.  
XX 04-AUG-2004; 2004US-00912534.  
XX 04-FEB-2004; 2004US-00772227.  
XX (VERB/) VERBSKY M L.  
XX (BAUB/) BAUBLITE C.  
XX (KLOE/) KLOEK A P.  
XX (DAVI/) DAVILA-APONTE J A.  
XX (HRES/) HRESKO M C.  
XX (MCLA/) MCLAIRD M B.  
XX (ZENT/) ZENTELLA R.  
XX (WILL/) WILLIAMS D J.  
XX Verbsky ML, Baublite C, Kloeck AP, Davila-Aponte JA, Hresko MC;  
XX MCLAIRD MB, Zentella R, Williams DJ;  
XX WPI; 2005-603337/62.  
XX N-PSDB; AEC02364.  
XX New transgenic plant having a DNA construct comprising a nucleic acid  
XX encoding a protein for catalyzing the conversion of a substrate to a C16,

PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
XX anhelmintic compounds.  
PS Claim 21; SEQ ID NO 136; 130pp; English.  
XX The invention relates to a transgenic plant containing at least one DNA  
CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
CC monounsaturated fatty acid product; and (b) a regulatory element operably  
CC linked to the nucleic acid encoding the polypeptide and conferring  
CC expression in a vegetative tissue of the plant. Also described: (1) a  
CC method of making a transgenic plant; (2) an isolated nucleic acid  
CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
CC construct comprising at least one regulatory element that confers  
CC expression in a vegetative tissue of a plant; and (4) a method of  
CC screening a transgenic plant for anhelmintic activity. The transgenic  
CC plant is useful in preparing compounds having anhelmintic activity. The  
CC present sequence represents an epoxigenase which is used in the  
CC exemplification of the present invention.  
XX Sequence 378 AA;  
SQ

Query Match 99.6%; Score 2077; DB 9; Length 378;  
Best Local Similarity 99.5%; Pred. No. 1.3e-214;  
Matches 376; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60  
Db 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60

Qy 61 YTVANTYIPLPPLVYLWVPVYFCQSCILTLGLWVLCGHCCHAFSEYQWIDNAGFVL 120  
Db 61 YTVANTYIPLPPLVYLWVPVYFCQSCILTLGLWVLCGHCCHAFSEYQWIDNAGFVL 120

Qy 121 HSALLTPVFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYVEFLDTPGRILILVI 180  
Db 121 HSALLTPVFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYVEFLDTPGRILILVI 180

Qy 181 MTLGFPPLLYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVPYGLKFLVQ 240  
Db 181 MTLGFPPLLYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVPYGLKFLVQ 240

Qy 241 TKFGVWCMYGVVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300  
Db 241 TKFGVWCMYGVVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300

Qy 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPIIGDYRMIDRTPPFKAMWREAKECIY 360  
Db 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPIIGDYRMIDRTPPFKAMWREAKECIY 360

Qy 361 IEQDADSKHKGTYYWHKM 378  
Db 361 IEQDADSKHKGTYYWHKM 378

RESULT 3  
AAW83354  
ID AAW83354 standard; protein; 384 AA.  
XX AAW83354;  
XX AAW83354;  
XX 27-AUG-2003 (revised)  
XX 10-FEB-1999 (first entry)  
XX Vernonia galamenensis fatty acid epoxidising enzyme.  
XX Vernonia galamenensis; fatty acid epoxidising enzyme.  
XX Vernonia galamenensis; fatty acid desaturase; epoxidising enzyme;  
XX expression; chimeric gene; recombinant enzyme.  
XX Vernonia galamenensis.  
XX US5846784-A.  
XX

PD 08-DEC-1998.  
XX 11-JUN-1997; 97US-00872302.  
XX 11-JUN-1997; 97US-00872302.  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Hitz WD;  
XX WPI; 1999-059065/05.  
XX N-PSDB; AAV72550.  
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid  
PT epoxidising enzyme - used to alter levels of expression of the enzymes in  
PT transformed host cells or to produce recombinant enzymes.  
XX Claim 5; Col 29-32; 21pp; English.  
XX The present sequence is Vernonia galamensis fatty acid epoxidising  
CC enzyme. The present invention also describes: (i) Vernonia galamensis  
CC fatty acid desaturase; (ii) chimeric genes comprising the fragments  
CC linked to regulatory sequences; and (iii) transformed host cells  
CC containing the chimeric genes. The DNA's from the present invention can  
CC be used to alter levels of expression of the enzymes in transformed host  
CC cells or to produce the recombinant enzymes by transformation of  
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)  
XX Sequence 384 AA;  
XX Query Match 87.3%; Score 1821; DB 2; Length 384;  
XX Best Local Similarity 84.3%; Pred. No. 5.3e-187;  
XX Matches 322; Conservative 29; Mismatches 27; Indels 4; Gaps 1;  
QY 1 MSDSYDDR----MKDHMDERAPIDPAPSLDLKKAIPAHCPRRSAAVWSSCVVQDLII 56  
DB 3 MSDSCDDHDLQKVDNINERAPVDAAFPSLDLKKAIPHCQFSAIRSSCVVQDLII 62  
QY 57 TFLTYVANTYIPLPPLVYLAWPVVWFCQSCILTGLWLGHECGHAFSEYQWIDNAV 116  
DB 63 TFLTYLANSYIPLPPLVYLAWPVVWFCQSSILTGLWLGHECGHAYSEYQWIDNV 122  
QY 117 GFVLHALLTPYFSWKYSHRKHANTNSLENEEVIYIPRTQSQRVSTYEFDLNTPGRIL 176  
DB 123 GFTLHSLTTPYFSWKYSHRKHANTNSLENEEVIYIPKAKSQLRYSNFKFLDNTGRI 182  
QY 177 ILVIMLTGFPPLVLLTNVSGKYDRFTNHFDPDLPSPFTFRERIOVALSDLGIVAVFVGLK 236  
DB 183 ILLIMLTGFPPLVLLTNISGKYQRPANHFDPDLPSPFISERERIQVVLSDVGLIAV 242  
QY 237 FLVOTKGFVWCMYGVVIGLNSFTIVITYLHHTLSPHVDSTENWIKGALTITDRD 296  
DB 243 FLVAKGFGVWVMYCAPVGLNAPLIMITYLHHTLSPHVDSTENWIKGALTITDRD 302  
QY 297 FGLNRFVHDVTHVTHLHLPYPIPHYHAKASEAIKPIGLDYRMDTRTPPFKAMWREAK 356  
DB 303 FGLNRFVHDVTHVTHLHLPYPIPHYHAKASEAIKPIGLDYRMDTRTPPFKAMWREAK 362  
QY 357 ECYIIEQDADSKHGKYVTHKM 378  
DB 363 ECYIIEPDEDKKGKYVTHKM 384  
RESULT 4  
AD8R7355  
ID ADR87355 standard; protein; 377 AA.  
XX  
XX ADR87355;  
XX  
XX 18-NOV-2004 (first entry)  
XX Hydroxylase/ epoxxygenase, SEQ ID 36.  
XX

KW Nematocide; Plant; 16C monounsaturated fatty acid;  
KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;  
KW fatty acid epoxxygenase; fatty hydroxylase; phospholipid:diacylglycerol;  
KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;  
KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;  
KW nematode.  
XX Stokesia laevis.  
OS  
XX WO2004071168-A2.  
PN  
XX 26-AUG-2004.  
XX  
XX 04-FEB-2004; 2004WO-US003254.  
PF  
XX 05-FEB-2003; 2003US-0445293P.  
PR  
XX (DIVE-) DIVERGENCE INC.  
PA  
XX Verbeke ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;  
PI Hresko MC, McIaird MB, Zentella R;  
XX  
XX WPI; 2004-634973/61.  
DR N-PSDB; ADR87346.  
XX  
XX Novel transgenic plant containing DNA construct having nucleic acid  
PT encoding polypeptide for catalyzing conversion of substrate to  
PT monounsaturated fatty acid product, useful for controlling nematodes.  
XX  
XX Claim 21; SEQ ID NO 36; 180pp; English.  
PS  
XX The present invention relates to transgenic plants (I) containing one or  
CC more DNA constructs. The DNA constructs have a nucleic acid encoding a  
CC protein effective for catalyzing the conversion of a substrate to a 16C,  
CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid  
CC epoxxygenase or a fatty hydroxylase, and a regulatory element operably  
CC linked to the nucleic acid encoding the protein, where the regulatory  
CC element confers expression in vegetative tissue of the plant. The fatty  
CC acid epoxxygenase or a fatty hydroxylase can be  
CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol  
CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty  
CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in  
CC a vegetative tissue. The DNA construct of (I) is useful in the production  
CC of hydroxylases and epoxxygenases that controls nematode damage in  
CC commercially important plant species and so (I) exhibits increased  
CC resistance to nematodes. (I) provides an effective, environmentally safe  
CC methods of inhibiting nematode metabolism, growth, viability,  
CC development, infectivity and/or the nematode life cycle. (I) provides  
CC season-long nematode control, thus providing labor savings, by reducing  
CC the need for and frequency of chemical control. The present sequence is  
CC one such fatty acid epoxxygenase and fatty hydroxylase used to illustrate  
CC the invention.  
XX  
XX Sequence 377 AA;  
QY Query Match 74.3%; Score 1549.5; DB 8; Length 377;  
XX Best Local Similarity 72.0%; Pred. No. 9.8e-158;  
XX Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;  
QY 1 MSDSYDDRMKDHMDERAPIDPAPSLDLKKAIPAHCPRRSAAVWSSCVVQDLITFLL 60  
DB 7 MSDLSDGK----NLLKRVDPD-PFTLSDIKKAIPHCPRRSVIRSYVVDLIVSYVF 61  
QY 61 YTVANTYIPLPPLVYLAWPVVWFCQSCILTGLWLGHECGHAFSEYQWIDNAVGFVL 120  
DB 62 FFLATYITVLPAFLAYIAVPVWFCQASILTGLWLGHECGHAFSEYQWIDTDTGFIL 121  
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIYIPRTQSQRVSTYEFDLNTPGRILILVI 180  
DB 122 HSALLTPYFSWKYSHRKHANTNSLENEEVIYIPKRSKYIYS--KILANPPGRVTLV 179  
QY 181 MLTGLFPPLVLLTNVSGKYDRFTNHFDPDLPSPFTFRERIOVALSDLGIVAVFVGLKFLVQ 240  
XX



Db 180 RLTLGFPPLVLLTNISGKKYQRPANHFDPPLSPFITERERIQVLVSDGLLAVIYAKLLVA 239  
 Qy 241 TKGFGWMCYGVPIGLNSPIIIVITLHHTHLSPPHYDSTENWIKGALTIDRDFGLL 300  
 Db 240 AKGAVWVTCIYGVPVLGVSVFVLITLHHTHLSLPHYDSTENWIRGALSTIDRDFGL 299  
 Qy 301 NRVFHDVTHVTHLHLLFPYIPIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 360  
 Db 300 NRVFHDVTHVTHLHLLISYIPIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 359  
 Qy 361 IEQDADSKHGKGYWYHKM 378  
 Db 360 IEPDEDEHKGYWYHKM 377

RESULT 5  
 ADR87357  
 ID ADR87357 standard; protein; 377 AA.  
 AC ADR87357;  
 DT 18-NOV-2004 (first entry)  
 XX Codon optimised hydroxylase/ epoxigenase, SEQ ID 38.  
 XX  
 XX Nematocide; Plant; 16C monounsaturated fatty acid;  
 KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;  
 KW fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;  
 KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;  
 KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;  
 KW nematode.  
 XX  
 XX Stokesia laevis.  
 OS Synthetic.  
 OS  
 PN WO2004071168-A2.  
 XX  
 XX 26-AUG-2004.  
 PD  
 PF 04-FEB-2004; 2004WO-US003254.  
 XX  
 XX 05-FEB-2003; 2003US-0445293P.  
 PR  
 XX (DIVE-) DIVERGENCE INC.  
 PA  
 XX Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;  
 PI Hresko MC, McLaird MB, Zentella R;  
 XX  
 DR WPI; 2004-634973/61.  
 DR N-P8DB; ADR87348.  
 XX  
 XX Novel transgenic plant containing DNA construct having nucleic acid  
 PT encoding polypeptide for catalyzing conversion of substrate to  
 PT monounsaturated fatty acid product, useful for controlling nematodes.  
 XX  
 XX Claim 21; SEQ ID NO 38; 180pp; English.  
 PS  
 CC The present invention relates to transgenic plants (I) containing one or  
 CC more DNA constructs. The DNA constructs have a nucleic acid encoding a  
 CC protein effective for catalyzing the conversion of a substrate to a 16C,  
 CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid  
 CC epoxigenase or a fatty hydroxylase, and a regulatory element operably  
 CC linked to the nucleic acid encoding the protein, where the regulatory  
 CC element confers expression in vegetative tissue of the plant. The fatty  
 CC acid epoxigenase or a fatty hydroxylase can be  
 CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol  
 CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty  
 CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in  
 CC a vegetative tissue. The DNA construct of (I) is useful in the production  
 CC of hydroxylases and epoxigenases that controls nematode damage in  
 CC commercially important plant species and so (I) exhibits increased  
 CC resistance to nematodes. (I) provides an effective, environmentally safe  
 CC methods of inhibiting nematode metabolism, growth, viability,

CC development, infectivity and/or the nematode life cycle. (I) provides  
 CC season-long nematode control, thus providing labor savings, by reducing  
 CC the need for and frequency of chemical control. The present sequence is  
 CC one such fatty acid epoxigenase and fatty hydroxylase, which has been  
 CC codon optimised for improved plant expression.  
 XX  
 SQ Sequence 377 AA;  
 Query Match 74.3%; Score 1549.5; DB 8; Length 377;  
 Best Local Similarity 72.0%; Pred. No. 9.8e-158;  
 Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;  
 Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLSDLKKAIPAHCFRESAVWSSCYVVDLIITFLL 60  
 Db 7 MSDLSGK---NLLKRPVDP--PFTLSDIKALPPHCFRKSVIRSSYYVVDLIVSYVF 61  
 Qy 61 YTVANTYIPHLPPPLVYLAWPVYWFQSCILITGLWVLGHECGHAFSEYQWIDNAVGVFL 120  
 Db 62 PFLATTYITVLPAPLAYIANPVYWFQASILITGLWVLGHECGHAFSEYQWIDDTVGFL 121  
 Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPRTQSLRTYTYSTYFELDNTPGRLILVI 180  
 Db 122 HSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRKSKVIYS--KILNPPGRVFTLVF 179  
 Qy 181 MLTGLPPLVLLTNVSGKKYDRFTNHPDPLSPFITERERIOVALSDLGIVAVFYGLKFLVQ 240  
 Db 180 RLTLGFPPLVLLTNISGKKYQRPANHFDPPLSPFITERERIOVLVSDGLLAVIYAKLLVA 239  
 Qy 241 TKGFGWMCYGVPIGLNSPIIIVITLHHTHLSPPHYDSTENWIKGALTIDRDFGLL 300  
 Db 240 AKGAVWVTCIYGVPVLGVSVFVLITLHHTHLSLPHYDSTENWIRGALSTIDRDFGL 299  
 Qy 301 NRVFHDVTHVTHLHLLFPYIPIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 360  
 Db 300 NRVFHDVTHVTHLHLLISYIPIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 359  
 Qy 361 IEQDADSKHGKGYWYHKM 378  
 Db 360 IEPDEDEHKGYWYHKM 377

RESULT 6  
 ADR87361  
 ID ADR87361 standard; protein; 377 AA.  
 AC ADR87361;  
 DT 18-NOV-2004 (first entry)  
 XX Codon optimised hydroxylase/ epoxigenase, SEQ ID 42.  
 XX  
 XX Nematocide; Plant; 16C monounsaturated fatty acid;  
 KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;  
 KW fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;  
 KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;  
 KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;  
 KW nematode.  
 XX  
 XX Stokesia laevis.  
 OS Synthetic.  
 OS  
 PN WO2004071168-A2.  
 XX  
 XX 26-AUG-2004.  
 PD  
 PF 04-FEB-2004; 2004WO-US003254.  
 XX  
 XX 05-FEB-2003; 2003US-0445293P.  
 PR  
 XX (DIVE-) DIVERGENCE INC.  
 PA  
 XX Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;  
 PI Hresko MC, McLaird MB, Zentella R;

```

XX WPI; 2004-634973/61.
DR N-PSDB; ADR87352.
XX
XX Novel transgenic plant containing DNA construct having nucleic acid
PT encoding polypeptide for catalyzing conversion of substrate to
PT monounsaturated fatty acid product, useful for controlling nematodes.
XX
XX Claim 21; SEQ ID NO 42; 180pp; English.
XX
XX The present invention relates to transgenic plants (I) containing one or
CC more DNA constructs. The DNA constructs have a nucleic acid encoding a
CC protein effective for catalyzing the conversion of a substrate to a 16C,
CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid
CC epoxigenase or a fatty hydroxylase, and a regulatory element operably
CC linked to the nucleic acid encoding the protein, where the regulatory
CC element confers expression in vegetative tissue of the plant. The fatty
CC acid epoxigenase or a fatty hydroxylase can be
CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol
CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty
CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in
CC a vegetative tissue. The DNA construct of (I) is useful in the production
CC of hydroxylases and epoxigenases that controls nematode damage in
CC commercially important plant species and so (I) exhibits increased
CC resistance to nematodes. (I) provides an effective, environmentally safe
CC methods of inhibiting nematode metabolism, growth, viability,
CC development, infectivity and/or the nematode life cycle. (I) provides
CC season-long nematode control, thus providing labor savings, by reducing
CC the need for and frequency of chemical control. The present sequence is
CC one such fatty acid epoxigenase and fatty hydroxylase, which has been
CC codon optimised for improved plant expression.
XX
XX Sequence 377 AA;
XX
Query Match 74.3%; Score 1549.5; DB 8; Length 377;
Best Local Similarity 72.0%; Pred. No. 9.8e-158;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;
QY 1 MDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPACFRPSAVWSSCVVQDLITFL 60
DB 7 MSLSGDK----NLLKRVDP--PFTSLDKKAIPHCFRSVIRSYVVDLIVSYVF 61
QY 61 YTVANTYIPLPPLVYLAWPVWFQSCILTLGLWLGHCGHAFSEYQWIDNAGFVL 120
DB 62 FFLATTYITVLPAPLAYIAWPVWFQASILTLGLWLGHCGHAFSEYQWIDTGVFIL 121
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFELDNTPGRIILVI 180
DB 122 HSALLTPYFSWKYSHRKHANTNSLNDDEVYIPKRKSKVIYS--KILANPPGRVFTLV 179
QY 181 MLTLGFPPLVLLTNVSGKGYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 240
DB 180 RLTLGFPPLVLLTNVSGKGYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 239
QY 241 TKGFGWCMYGPVIGLANSFIIVITLHHTLSSPHYDSTENWNWIKGALTITDRDGLL 300
DB 240 AKGAVWTCIYGPVLGVSVEFLITVHLHTLSLPHYDSTENWNWIRGALSTIDRDFGL 299
QY 301 NRVFHDVTHVHLHLPPIYPHYHAKASEAIPILGDYRMDIRTPFFKAWREAKECIY 360
DB 300 NRVFHDVTHVHLHLISYIPHYHAKEARDAIKPVLGDYKIDRTPIFKAWREAKECIY 359
QY 361 IEODADSKHGTYVYHKM 378
DB 360 IEPEDETEHKGVYVYHKM 377
RESULT 7
ID AEC02271 standard; protein; 377 AA.
XX
XX AEC02271;
XX

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DT 06-OCT-2005 (first entry)
XX
XX Stokesia laevis epoxigenase SEQ ID NO:38.
XX
XX transgenic plant; anthelmintic; epoxigenase.
XX
XX Stokesia laevis.
XX
XX US2005172358-A1.
XX
XX 04-AUG-2005.
XX
XX 04-AUG-2004; 2004US-00912534.
XX
XX 04-FEB-2004; 2004US-00772227.
XX
XX (VERB/) VERBSKY M L.
XX (BAUB/) BAUBLITE C.
XX (KLOE/) KLOEK A P.
XX (DAVI/) DAVILA-APONTE J A.
XX (HRES/) HRESKO M C.
XX (MCLA/) MCLAIRD M B.
XX (ZENT/) ZENTELLA R.
XX (WILL/) WILLIAMS D J.
XX
XX Verbesky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;
PI Mcclaird MB, Zentella R, Williams DJ;
XX
XX WPI: 2005-603337/62.
XX N-PSDB; AEC02262.
XX
XX New transgenic plant having a DNA construct comprising a nucleic acid
PT encoding a protein for catalyzing the conversion of a substrate to a C16,
PT C18 or C20 monounsaturated fatty acid product, useful in preparing
PT anthelmintic compounds.
XX
XX Claim 21; SEQ ID NO 38; 130pp; English.
XX
XX The invention relates to a transgenic plant containing at least one DNA
CC construct comprising: (a) a nucleic acid encoding a polypeptide effective
CC for catalyzing the conversion of a substrate to a C16, C18, or C20
CC monounsaturated fatty acid product; and (b) a regulatory element operably
CC linked to the nucleic acid encoding the polypeptide and conferring
CC expression in a vegetative tissue of the plant. Also described: (1) a
CC method of making a transgenic plant; (2) an isolated nucleic acid
CC comprising the nucleotide sequence; (3) a recombinant nucleic acid
CC construct comprising at least one regulatory element that confers
CC expression in a vegetative tissue of a plant; and (4) a method of
CC screening a transgenic plant for anthelmintic activity. The transgenic
CC plant is useful in preparing compounds having anthelmintic activity. The
CC present sequence represents an epoxigenase which is used in the
CC exemplification of the present invention.
XX
XX Sequence 377 AA;
XX
Query Match 74.3%; Score 1549.5; DB 9; Length 377;
Best Local Similarity 72.0%; Pred. No. 9.8e-158;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;
QY 1 MDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPACFRPSAVWSSCVVQDLITFL 60
DB 7 MSLSGDK----NLLKRVDP--PFTSLDKKAIPHCFRSVIRSYVVDLIVSYVF 61
QY 61 YTVANTYIPLPPLVYLAWPVWFQSCILTLGLWLGHCGHAFSEYQWIDNAGFVL 120
DB 62 FFLATTYITVLPAPLAYIAWPVWFQASILTLGLWLGHCGHAFSEYQWIDTGVFIL 121
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFELDNTPGRIILVI 180
DB 122 HSALLTPYFSWKYSHRKHANTNSLNDDEVYIPKRKSKVIYS--KILANPPGRVFTLV 179
QY 181 MLTLGFPPLVLLTNVSGKGYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 240

```

Db 180 RLTGLFPYLLTNTSGKKYQRFANHFDPISPIFTRERIQVLVSDGLLAVIYAIKLVA 239

Qy 241 TKGFGWVMCMYGVPIVGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300

Db 240 AKGAVWVTCIYGVPLVGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299

Qy 301 NRVFHDVTHVHLHLPYIPIHYHAKSEAIKPTILGDRMIDRTPPFKAMWREAKECIY 360

Db 300 NRVFHDVTHVHLHLLSYIPIHYHAKSEARDAIKPVLGDYKYIDRTPIPKAMWREAKECIY 359

Qy 361 IEQADSKHGKTYWYHKM 378

Db 360 IEPDEDETHKGVYWHKM 377

RESULT 8

AC AEC02275

DE AEC02275 standard; protein; 377 AA.

DT 06-OCT-2005 (first entry)

DE Stokesia laevis epoxigenase SEQ ID NO:42.

XX transgenic plant; anthelmintic; epoxigenase.

OS Stokesia laevis.

XX US2005172358-A1.

XX 04-AUG-2005.

PF 04-AUG-2004; 2004US-00912534.

PR 04-FEB-2004; 2004US-00772227.

PA (VERB/) VERBSKY M L.

PA (BAUB/) BAUBLITE C.

PA (KLOE/) KLOEK A P.

PA (DAVI/) DAVILA-APONTE J A.

PA (HRES/) HRESKO M C.

PA (MCLA/) MCLAIRD M B.

PA (ZENT/) ZENTELLA R.

PA (WILL/) WILLIAMS D J.

XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC; Mclaird MB, Zentella R, Williams DJ;

XX WPI; 2005-603337/62.

XX N-PSDB; AEC02266.

PT New transgenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a C16, C18 or C20 monounsaturated fatty acid product, useful in preparing anthelmintic compounds.

XX Claim 21; SEQ ID NO 42; 130pp; English.

XX The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The present sequence represents an epoxigenase which is used in the exemplification of the present invention.

XX SQ Sequence 377 AA;

Query Match 74.3%; Score 1549.5; DB 9; Length 377;

Best Local Similarity 72.0%; Pred. No. 9.8e-158;

Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSYDORMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVSSCYVQDLIITFLL 60

Db 7 MSDSLSDGK---NLLKRVVPDP-EFTLSIDIKKAIPPHCFRKSVIRSSYYVHDLIVSYVF 61

Qy 61 YTVANTYIPLPPLVYLAWPVYFVFCOSCIITGLWLGHEGCHHAFSEYQWIDNAVGFV 120

Db 62 PFLATTITVLPAPLAYIANPVYFVFCQASILTGLWLGHEGCHHAFSEYQWIDTGVF 121

Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEVYIPRTQSLRTYSTYFELDNTPPGRILILVI 180

Db 122 HSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRKVKIYS--KIINPPGRVFTLVF 179

Qy 181 MLTGLFPYLLTNTSGKKYQRFANHFDPISPIFTRERIQVLVSDGLLAVIYAIKLVA 240

Db 180 RLTGLFPYLLTNTSGKKYQRFANHFDPISPIFTRERIQVLVSDGLLAVIYAIKLVA 239

Qy 241 TKGFGWVMCMYGVPIVGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300

Db 240 AKGAVWVTCIYGVPLVGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299

Qy 301 NRVFHDVTHVHLHLPYIPIHYHAKSEAIKPTILGDRMIDRTPPFKAMWREAKECIY 360

Db 300 NRVFHDVTHVHLHLLSYIPIHYHAKSEARDAIKPVLGDYKYIDRTPIPKAMWREAKECIY 359

Qy 361 IEQADSKHGKTYWYHKM 378

Db 360 IEPDEDETHKGVYWHKM 377

RESULT 9

AC AEC02269

DE AEC02269 standard; protein; 377 AA.

DT 06-OCT-2005 (first entry)

DE Stokesia laevis epoxigenase SEQ ID NO:36.

XX transgenic plant; anthelmintic; epoxigenase.

OS Stokesia laevis.

XX US2005172358-A1.

XX 04-AUG-2005.

PF 04-AUG-2004; 2004US-00912534.

PR 04-FEB-2004; 2004US-00772227.

PA (VERB/) VERBSKY M L.

PA (BAUB/) BAUBLITE C.

PA (KLOE/) KLOEK A P.

PA (DAVI/) DAVILA-APONTE J A.

PA (HRES/) HRESKO M C.

PA (MCLA/) MCLAIRD M B.

PA (ZENT/) ZENTELLA R.

PA (WILL/) WILLIAMS D J.

XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC; Mclaird MB, Zentella R, Williams DJ;

XX WPI; 2005-603337/62.

XX N-PSDB; AEC02260.

PT New transgenic plant having a DNA construct comprising a nucleic acid  
 PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
 PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anthelmintic compounds.

PS Claim 21; SEQ ID NO 36; 130pp; English.

XX The invention relates to a transgenic plant containing at least one DNA  
 CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
 CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
 CC monounsaturated fatty acid product; and (b) a regulatory element operably  
 CC linked to the nucleic acid encoding the polypeptide and conferring  
 CC expression in a vegetative tissue of the plant. Also described: (1) a  
 CC method of making a transgenic plant; (2) an isolated nucleic acid  
 CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
 CC construct comprising at least one regulatory element that confers  
 CC expression in a vegetative tissue of a plant; and (4) a method of  
 CC screening a transgenic plant for anthelmintic activity. The transgenic  
 CC plant is useful in preparing compounds having anthelmintic activity. The  
 CC present sequence represents an epoxigenase which is used in the  
 CC exemplification of the present invention.

XX Sequence 377 AA;

Query Match 74.3%; Score 1549.5; DB 9; Length 377;

Best Local Similarity 72.0%; Pred. No. 9.8e-158;

Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

QY 1 MSDSYDRMKDHMDRERAPIDPAPFSLDLKKAIPACFRSRAVSSCVVQDLITFL 60

DB 7 MSLSDBGK----NLLKRVVPDP--PFTLSIDIKKAIPPCFKRSVRSYVVDLIVSYVF 61

QY 61 YTVANTYIPLHPPLVYLAWPVWFQSCILTLGLWLGHCCHGHPFSEYQWIDNAVGFVL 120

DB 62 FFLATYITVLPALYIAWPVWFQASILTGLWLGHCCHGHPFSEYQWIDDTVGFL 121

QY 121 HSALLTPFSWKYSHRKHANTNSLENEEVIPTQSLRTYSTYFELDNTPGRIILVI 180

DB 122 HSALLTPFSWKYSHRKHANTNSLDNDEVYIPKRSKVKIYS--KILNPPGRVFTLVF 179

QY 181 MLTLGPLYLLTNVSGKKYDRFTNHPDLSPIFTEERIOVALSDLGIVAFGLFLVQ 240

DB 180 RLTLGPLYLLTNISGKKYQRFANHPDLSPIFTEERIOQLVSDLGLLAVIAKLLVA 239

QY 241 TKGFGWCMYGPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRFGLL 300

DB 240 AKGAVWTCYGVPLGVSVFVLIITYLHHTLSSPHYDSTENWIRGALSTIDRFGFL 299

QY 301 NRVFHDVTHVLHLLFPYIPHYHAKSEAIKPILGDMIDRTPTFFKAMWREAKECIY 360

DB 300 NRVFHDVTHVLHLLISYIPHYHAKSEAIKPIVLGDYIKIDRTPTIFKAMWREAKECIY 359

QY 361 IEODASKKNGTYYHKM 378

DB 360 IEPEDETEHKGVYVYHKM 377

RESULT 10

AAB70946

ID AAB70946 standard; protein; 377 AA.

XX

AC AAB70946;

XX

DT 22-AUG-2001 (first entry)

XX

DE C. officinalis calendulic acid desaturase.

KW

KX Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;

KW triglyceride; transgenic plant.

XX

OS Calendula officinalis.

XX

PN DE19941609-A1.

XX 08-MAR-2001.

PD 01-SEP-1999; 99DE-01041609.

PF 01-SEP-1999; 99DE-01041609.

PR 01-SEP-1999; 99DE-01041609.

XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.

XX Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;

XX WPI: 2001-283028/30.

XX N-PSDB; AAF88311.

XX New nucleic acid sequence encoding Calendula officinalis calendulic acid

XX desaturase, useful for e.g. producing transgenic plants having oil with

XX an increased unsaturated fatty acid content.

XX Claim 1c; Page 15-16; 22pp; German.

XX This invention describes a novel isolated nucleic acid sequence (I)  
 CC encoding a Calendula officinalis calendulic acid desaturase polypeptide.  
 CC The invention also describes (I) a process for producing unsaturated  
 CC fatty acids, comprising introducing at least one copy of (I) or (II) into  
 CC an oil-producing organism, growing the organism, isolating oil from the  
 CC organism and releasing fatty acids from the oil; (2) a process for  
 CC producing triglycerides with an increased unsaturated fatty acid content,  
 CC comprising introducing at least one copy of (I) or (II) into an oil-  
 CC producing organism, growing the organism and isolating oil from the  
 CC organism; (3) a process for producing saturated fatty acids, comprising  
 CC introducing at least one nonfunctional copy of (I) or (II) into an oil-  
 CC producing organism, growing the organism, isolating oil from the organism  
 CC and releasing fatty acids from the oil; (4) a process for producing  
 CC triglycerides with an increased saturated fatty acid content, comprising  
 CC introducing at least one nonfunctional copy of (I) or (II) into an oil-  
 CC producing organism, growing the organism and isolating oil from the  
 CC organism; (5) an enzyme capable of converting a diunsaturated fatty acid  
 CC of to a triunsaturated fatty acid. Transgenic organisms (especially  
 CC plants) containing one or more copies of (I) are useful for producing  
 CC oils with an increased unsaturated fatty acid content. Transgenic  
 CC organisms (especially plants) containing one or more nonfunctional copies  
 CC of (I) are useful for producing oils with an increased saturated fatty  
 CC acid content. (I) and fragments of (I) are also useful for isolating  
 CC genomic sequences by homology screening. This sequence represents the  
 CC calendulic acid desaturase described in the method of the invention

XX Sequence 377 AA;

Query Match

Best Local Similarity 73.0%; Score 1523.5; DB 4; Length 377;

Matches 269; Conservative 45; Mismatches 54; Indels 7; Gaps 3;

QY 8 RMKD----HMDERAPIDPAPFSLDLKKAIPACFRSRAVSSCVVQDLITFLTYTV 63

DB 6 RMSDPSEGNILERVDP--PFTLSDLKKAIPACFRSRAVSSCVVQDLITFLTYTV 64

QY 64 ANTYIPLHPPLVYLAWPVWFQSCILTLGLWLGHCCHGHPFSEYQWIDNAVGFVLHSA 123

DB 65 ANTYIPLHPPLVYLAWPVWFQSCILTLGLWLGHCCHGHPFSEYQWIDNAVGFVLHSA 124

QY 124 LLTPYFSWKYSHRKHANTNSLENEEVIPTQSLRTYSTYFELDNTPGRIILVIMLT 183

DB 125 LLTPYFSWKYSHRKHANTNSLDNDEVYIPKRSKVKIYS--KILNPPGRVFTLVFRLT 182

QY 184 LGFPLYLLTNVSGKKYDRFTNHPDLSPIFTEERIOVALSDLGIVAFGLFLVOTKG 243

DB 183 LGFPLYLLTNISGKKYGRFANHPDMSPIFNDRERVQVLLSDPGLAVFAYAKLLVAAG 242

QY 244 FGWVCMYGPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDGFGLNRV 303

DB 243 AAWVINMYAIPVIGSVFVLIITYLHHTLSSPHYDSTENWIKGALTITDRDGFGLNRV 302

QY 304 FHDVTHVLHLLFPYIPHYHAKSEAIKPILGDMIDRTPTFFKAMWREAKECIYIEQ 363

Db 303 FHDVTHVHLHLISYIIPHYHAKARDAIKPVLGEYKIDTPIPKAMREAKECIIYEP 362  
 QY 364 DADSKHGTYWYHKM 378  
 Db 363 DEDSEHKGFWYHKM 377

## RESULT 11

AAW79743  
 ID AAW79743 standard; protein; 374 AA.

XX AC AAW79743;

DT 02-FEB-1999 (first entry)

XX DE Crepis sp. delta-12-epoxygenase.

KW Fatty acid epoxygenase; CrepX gene; delta-12-epoxygenase;  
 KW mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;  
 KW vegetable oil; oilseed.

XX OS Crepis sp.

XX FH Location/Qualifiers

FT Key 99..104

FT Region /note= "His-rich region"

FT Region 135..139

FT Region /note= "His-rich region"

FT Misc-difference 293

FT /note= "encoded by AGN"

FT Misc-difference 305

FT /note= "encoded by GTN"

FT Region 309..313

FT /note= "His-rich region"

XX WO9846762-A1.

XX PD 22-OCT-1998.

XX PF 09-APR-1998; 98WO-AU000246.

XX PR 15-APR-1997; 97AU-00006223.

XX PR 15-APR-1997; 97AU-00006226.

XX PR 16-APR-1997; 97US-0043706P.

XX PR 20-JUN-1997; 97US-0050403P.

XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX PA (STYK/) STYMNE S.

XX PI Stymne S, Green A, Singh S, Lenman M;

XX WPI; 1998-568734/48.

XX DR N-PSDB; AAW63102.

XX New isolated fatty acid epoxygenase gene - used particularly for

PT transforming plants for producing modified oils for use in, e.g.

PT coatings, resins, glues, plastics, surfactants or lubricants.

XX Claim 29; Page 84-86; 150pp; English.

XX This is the amino acid sequence of a novel epoxygenase of a vernolic acid

CC -containing Crepis sp. (not crepis palaestina). It was deduced from

CC isolated cDNA clone CrepX (see AAW63102). The deduced sequence contains

CC His-rich motifs (see AAW79752-54) that are characteristic of mixed

CC function monooxygenases, and shows a high degree of homology to a novel

CC delta-12-epoxygenase (see AAW79742) of C. palaestina. The invention

CC relates generally to novel genetic sequences (see AAW63101-03) encoding

CC fatty acid epoxygenases (see AAW79742-44), especially delta-12-

CC epoxygenases or mixed function monooxygenases. These provide the means by

CC which fatty acid metabolism can be manipulated in e.g. yeast, mould,

CC bacteria, insects, birds, mammals and plants (especially oilseed plants

CC such as flax), in particular to convert unsaturated fatty acids to

CC epoxygenated fatty acids. The invention includes genetically modified oil

CC -accumulating organisms and to the oils derived from them. These oils can

CC be used in production of coatings, resins, glues, plastics, surfactants

XX or lubricants

XX Sequence 374 AA;

Query Match 72.4%; Score 1510; DB 2; Length 374;

Best Local Similarity 70.4%; Pred. No. 1.8e-153;

Matches 261; Conservative 50; Mismatches 56; Indels 4; Gaps 2;

QY 8 RMKDHDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVVQDLIIITELLYTVANTY 67

Db 8 RTSEKSVMERVSVDPTVTFSLDLKQAIPPHCFQSRVIRSSVVVQDLIIAIFYFLANTY 67

QY 68 IPHLPPLVYLAWPVYWFQSCILITGLWVLGHEGCHHAFSEYQWIDNAVGVLSHALLTP 127

Db 68 IPNLPHPLAYLAWPLYWFCQASVLTGLWILGHEGCHHAYSNTWVDDTVGFIHSLFLTP 127

QY 128 YFSWKYSHRKHHTNSLENEEVYIPKTSQRLRTYSTYEFLDNTPGRIILILVIMLTGLFP 187

Db 128 YFSWKYSHRNHHSNTSSIDNDENVYIPKSKLKL--RIYKLNPPGRLLVLVIMLTGLFP 185

QY 188 LYLLTNVSGKKYDRFTNHFDPLSPFTERRIQVALSDLGIVAVFYGLKFLVQTKGCGW 247

Db 186 LYLLTNISGKKYDRFANHFDPMSPIFKEREPFQVFLSDGLLAVFYGLKAVANKGAAMV 245

QY 248 MCMYGVPIGNSFIIVITLHHTLSPHYDSTEWNIKALTTIDRDFGLLNVRVHDV 307

Db 246 ACMYGVPLGVTFDFVITFLHHTHQSPPHYDSTEWNIKALTTIDRDFGLNVRVHDV 305

QY 308 THTHVLHPLPYIIPHYHAKASEAIKPLGDYRMIDRTPPFKAMWREAKECIIYEQDADS 367

Db 306 THTHVMHPLFSYIIPHYHAKEARDAIKPLGDYFYMIDRTPILKAMWREGRECMIYE--PDS 363

QY 368 KHKGTYWYHKM 378

Db 364 KLKGVYVYHKL 374

## RESULT 12

ADR87360

ID ADR87360 standard; protein; 374 AA.

XX AC ADR87360;

XX DT 18-NOV-2004 (first entry)

XX DE Codon optimised hydroxylase/ epoxygenase, SEQ ID 41.

XX KW Nematocide; plant; 16C monounsaturated fatty acid;

XX KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;

XX KW fatty acid epoxygenase; fatty hydroxylase; phospholipid:diacylglycerol;

XX KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;

XX KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;

XX KW nematode.

XX OS Crepis biennis.

XX OS Synthetic.

XX PN WO2004071168-A2.

XX PD 26-AUG-2004.

XX PF 04-FEB-2004; 2004WO-US003254.

XX PR 05-FEB-2003; 2003US-0445293P.

XX PA (DIVE-) DIVERGENCE INC.

XX Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;

XX PI Hresko MC, Mc Laird MB, Zentella R;

XX

DR WPI; 2004-634973/61.  
 XX N-PSDB; ADR87351.  
 PT Novel transgenic plant containing DNA construct having nucleic acid  
 PT encoding polypeptide for catalyzing conversion of substrate to  
 PT monounsaturated fatty acid product, useful for controlling nematodes.  
 XX  
 PS Claim 21; SEQ ID NO 41; 180pp; English.  
 XX  
 CC The present invention relates to transgenic plants (I) containing one or  
 CC more DNA constructs. The DNA constructs have a nucleic acid encoding a  
 CC protein effective for catalyzing the conversion of a substrate to a 16C,  
 CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid  
 CC epoxigenase or a fatty hydroxylase, and a regulatory element operably  
 CC linked to the nucleic acid encoding the protein, where the regulatory  
 CC element confers expression in vegetative tissue of the plant. The fatty  
 CC acid epoxigenase or a fatty hydroxylase can be  
 CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol  
 CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty  
 CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in  
 CC a vegetative tissue. The DNA construct of (I) is useful in the production  
 CC of hydroxylases and epoxigenases that controls nematode damage in  
 CC commercially important plant species and so (I) exhibits increased  
 CC resistance to nematodes. (II) provides an effective, environmentally safe  
 CC methods of inhibiting nematode metabolism, growth, viability,  
 CC development, infectivity and/or the nematode life cycle. (I) provides  
 CC season-long nematode control, thus providing labor savings, by reducing  
 CC the need for and frequency of chemical control. The present sequence is  
 CC one such fatty acid epoxigenase and fatty hydroxylase, which has been  
 CC codon optimised for improved plant expression.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 72.1%; Score 1504; DB 8; Length 374;  
 Best Local Similarity 69.0%; Pred. No. 7.9e-153;  
 Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;  
 QY 1 MSDSDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 Db 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 QY 61 YTVANTYIPLPPPLVLAWPVWFQSCILTLGLWLGHECGHAFSEYQWIDNAGFVL 120  
 Db 61 YFLADKYIPILPAFLAYLAWPLWFCQASILTGLWLGHECGHAFSEYQWIDNAGFVL 120  
 QY 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 180  
 Db 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 180  
 QY 178 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 178  
 Db 178 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 178  
 QY 181 MLTGLFPYLLTNVSGKDYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQ 240  
 Db 181 MLTGLFPYLLTNVSGKDYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQ 240  
 QY 241 TKGFGVMCMGVPIVGLNSFIIVITLHHTLSSPHYSTENWTKGALTIDRDPGLL 300  
 Db 239 KKGAAWVACVGVPMGLGVFTLFDIITLHHTQSSPHYSTENWTKGALTIDRDPGLL 298  
 QY 301 NRVFHDVTHVLHLFPPIPHYHAKASEAIKPIGLDYMIDRTPTFFKAMWREACEKY 360  
 Db 299 NSVFHDVTHVLHMFSPPIPHYHAKARDAINIIGDYIMIDRTPTILKALWREACEKY 358  
 QY 361 IEQDADSCKGTWYHKM 378  
 Db 359 IE--PDSKRGVYWKHL 374  
 RESULT 13  
 AEC02274  
 ID AEC02274 standard; protein; 374 AA.  
 XX  
 AC AEC02274;  
 XX  
 DT 06-OCT-2005 (first entry)

XX DE Crepis biennis epoxigenase SEQ ID NO:41.  
 XX transgenic plant; anthelmintic; epoxigenase.  
 KW Crepis biennis.  
 OS Synthetic.  
 OS  
 XX US2005172358-A1.  
 XX  
 PD 04-AUG-2005.  
 XX  
 PF 04-AUG-2004; 2004US-00912534.  
 XX  
 PR 04-FEB-2004; 2004US-00772227.  
 XX  
 PA (VERB/) VERBSKY M L.  
 PA (BAUB/) BAUBLITE C.  
 PA (KLOE/) KLOEK A P.  
 PA (DAVI/) DAVILA-APONTE J A.  
 PA (HRES/) HRESKO M C.  
 PA (MCLA/) MCLAIRD M B.  
 PA (ZENT/) ZENTELLA R.  
 PA (WILL/) WILLIAMS D J.  
 XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
 PI Mclaird MB, Zentella R, Williams DJ;  
 XX  
 DR WPI: 2005-603337/62.  
 DR N-PSDB; AEC02265.  
 XX  
 PT New transgenic plant having a DNA construct comprising a nucleic acid  
 PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
 PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anthelmintic compounds.  
 XX  
 PS Claim 21; SEQ ID NO 41; 130pp; English.  
 XX  
 CC The invention relates to a transgenic plant containing at least one DNA  
 CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
 CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
 CC monounsaturated fatty acid product; and (b) a regulatory element operably  
 CC linked to the nucleic acid encoding the polypeptide and conferring  
 CC expression in a vegetative tissue of the plant. Also described: (1) a  
 CC method of making a transgenic plant; (2) an isolated nucleic acid  
 CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
 CC construct comprising at least one regulatory element that confers  
 CC expression in a vegetative tissue of a plant; and (4) a method of  
 CC screening a transgenic plant for anthelmintic activity. The transgenic  
 CC plant is useful in preparing compounds having anthelmintic activity. The  
 CC present sequence represents an epoxigenase which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 72.1%; Score 1504; DB 9; Length 374;  
 Best Local Similarity 69.0%; Pred. No. 7.9e-153;  
 Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;  
 QY 1 MSDSDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 Db 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 QY 61 YTVANTYIPLPPPLVLAWPVWFQSCILTLGLWLGHECGHAFSEYQWIDNAGFVL 120  
 Db 61 YFLADKYIPILPAFLAYLAWPLWFCQASILTGLWLGHECGHAFSEYQWIDNAGFVL 120  
 QY 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 180  
 Db 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 180  
 QY 178 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 178  
 Db 178 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQRLTYSTYFELDNTGRIILVI 178  
 QY 181 MLTGLFPYLLTNVSGKDYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQ 240  
 Db 181 MLTGLFPYLLTNVSGKDYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQ 240





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GenCore version 5.1.9  
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- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	60.5	383	7	US-11-056-355B-52712 Sequence 52712, A
2	1215	58.2	377	7	US-11-056-355B-39929 Sequence 39929, A
3	1215	58.2	377	7	US-11-056-355B-42537 Sequence 42537, A
4	1215	58.2	377	7	US-11-056-355B-75575 Sequence 75575, A
5	1215	58.2	377	7	US-11-056-355B-98547 Sequence 98547, A
6	1215	58.2	377	7	US-11-056-355B-109786 Sequence 109786, A
7	1215	58.2	383	7	US-11-058-746-6 Sequence 6, Appli
8	1215	58.2	383	7	US-11-056-355B-39928 Sequence 39928, A
9	1215	58.2	383	7	US-11-056-355B-42536 Sequence 42536, A
10	1215	58.2	383	7	US-11-056-355B-75574 Sequence 75574, A
11	1215	58.2	383	7	US-11-056-355B-98546 Sequence 98546, A
12	1215	58.2	383	7	US-11-056-355B-109785 Sequence 109785, A
13	1214	58.2	377	7	US-11-056-355B-28876 Sequence 28876, A
14	1214	58.2	377	7	US-11-056-355B-24466 Sequence 24466, A
15	1214	58.2	383	7	US-11-056-355B-28875 Sequence 28875, A
16	1214	58.2	383	7	US-11-056-355B-32465 Sequence 32465, A
17	1205.5	57.8	384	7	US-11-340-318-6 Sequence 6, Appli
18	1192	57.1	387	7	US-11-058-746-5 Sequence 5, Appli
19	1191.5	57.1	384	7	US-11-340-318-2 Sequence 2, Appli
20	1187.5	56.9	384	7	US-11-340-318-4 Sequence 4, Appli
21	1186.5	56.9	384	7	US-11-058-746-4 Sequence 4, Appli
22	1146	54.9	384	7	US-11-058-746-7 Sequence 7, Appli
23	1137	54.5	390	6	US-10-449-902-48623 Sequence 48623, A
24	1133	54.3	388	6	US-10-449-902-43123 Sequence 43123, A
25	1127	54.0	381	6	US-10-953-349-28921 Sequence 28921, A

RESULT 1

US-11-056-355B-52712  
; Sequence 52712, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 52712  
; LENGTH: 383  
; TYPE: prt  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(383)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177299  
US-11-056-355B-52712

Query Match 60.5%; Score 1263; DB 7; Length 383;  
Best Local Similarity 58.1%; Pred. No. 7.5e-108;  
Matches 215; Conservative 66; Mismatches 87; Indels 2; Gaps 1;

QY	7	DRMKDHMDERAPI	PAPPSLDLKAIPA	FRRAVWSSCVVODLITFLLYVANT	66
DB	13	NRKSEYDPLKRV	VPFEPKPPFSLQIKKVI	PPHCFQSFVSFVSVDLTIAFLCYVATH	72
QY	67	YIPLPPPLVYLAW	PYVWECOSCLTGLV	LGHGCHAFSEYQWIDNAGFVLHSA	126
DB	73	YFHLPLSFLSL	FLAWPYWAVQGCILTV	WVWIAHCGHAFSDYQLDDIIVLHSG	132
QY	127	PYFSWKYSHRKH	ANTNSLENEBEVPIPT	QSOLRTYSTVEFLDNTPGRIILVIM	186
DB	133	PYFSWKYSHRHH	NTSGSLERDEVFPVK	QKSKIKWSKY--LNNPGRVLTAV	190
QY	187	PYLLTNVSGKY	DRPTNHPDPLSPIT	FRERIOVALSDLGIVAVPYGLKFL	246
DB	191	PLYLALNVSGR	PYDRFACHYDPG	PIYSRRLQIYISDAGVLAVCYGL	250
QY	247	VMCMGVPIGLN	SFIIVITLHHHLS	SPHYDSTENWIKGALTIDRFG	306
DB	251	VVCVGVPLLV	VNNGFLVLTITF	LQHTHPALPHYTSSSEWDLRG	310

ALIGNMENTS

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QY 307 VTHVHLHLPPYIPHYHAKSEAIKPILDYRMIDRTPFKAMWREAKECIYEQDAD 366
Db 311 ITDTHVAHHLFSTMPHYHAMEATKAIPKILGEYVRFDETFPVKAMWREARECIYVDPQS 370
QY 367 SKHKGTYWYH 376
Db 371 TESKGVFWYN 380

RESULT 2
US-11-056-355B-39929
; Sequence 39929, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 39929
; LENGTH: 377
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 12370301
US-11-056-355B-39929

Query Match 58.2%; Score 1215; DB 7; Length 377;
Best Local Similarity 55.6%; Pred. No. 1.8e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDMDERAPIDPAPPSLSDLKKAIPAHCFRRSAVSSCYVVDLIITFLTYVANTY 67
Db 8 KKSETDTTKRVPCPKPPFSGVGLKKAIPPHCFKRSIPRFSYLSIDIIIIASCYYVATNY 67
QY 68 IPHLPPLVYLAWPYVWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 68 FSLLPQPLSYLAWPLYWACQCGVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLVLP 127
QY 128 YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTPGRILILVIMLTGFP 187
Db 128 YFSWKYSHRRHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185
QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQTKGFGWV 247
Db 186 LYLAFNVSGRPYDGFACHFFPNAPYNDREKLQIYLSDAGILAVCFGLYRYAAAGQMASM 245
QY 248 MCMYGVPIVGLNSFIIVITYLHHTHLSPHYDSTENWIKGALTITIDRDFGLLNRFHDV 307
Db 246 ICLYGVPLLIIVNAFLVLTIVLQHTHPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 305
QY 308 THTVHLHLPPYIPHYHAKSEAIKPILDYRMIDRTPFKAMWREAKECIYEQDADS 367
Db 306 TDTVAHHLFSTMPHYNAMEATKAIPKILGDYIQFDGTPWYVAMYREAKECIYVSPDREG 365
QY 368 KHKGTYWYH 376
Db 366 DKKGYYWYN 374

RESULT 4
US-11-056-355B-75575
; Sequence 75575, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 75575
; LENGTH: 377
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
```

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QY 307 VTHVHLHLPPYIPHYHAKSEAIKPILDYRMIDRTPFKAMWREAKECIYEQDAD 366
Db 311 ITDTHVAHHLFSTMPHYHAMEATKAIPKILGEYVRFDETFPVKAMWREARECIYVDPQS 370
QY 367 SKHKGTYWYH 376
Db 371 TESKGVFWYN 380

RESULT 2
US-11-056-355B-39929
; Sequence 39929, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 39929
; LENGTH: 377
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 12370301
US-11-056-355B-39929

Query Match 58.2%; Score 1215; DB 7; Length 377;
Best Local Similarity 55.6%; Pred. No. 1.8e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDMDERAPIDPAPPSLSDLKKAIPAHCFRRSAVSSCYVVDLIITFLTYVANTY 67
Db 8 KKSETDTTKRVPCPKPPFSGVGLKKAIPPHCFKRSIPRFSYLSIDIIIIASCYYVATNY 67
QY 68 IPHLPPLVYLAWPYVWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 68 FSLLPQPLSYLAWPLYWACQCGVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLVLP 127
QY 128 YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTPGRILILVIMLTGFP 187
Db 128 YFSWKYSHRRHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185
QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAFYGLKFLVQTKGFGWV 247
Db 186 LYLAFNVSGRPYDGFACHFFPNAPYNDREKLQIYLSDAGILAVCFGLYRYAAAGQMASM 245
QY 248 MCMYGVPIVGLNSFIIVITYLHHTHLSPHYDSTENWIKGALTITIDRDFGLLNRFHDV 307
Db 246 ICLYGVPLLIIVNAFLVLTIVLQHTHPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 305
QY 308 THTVHLHLPPYIPHYHAKSEAIKPILDYRMIDRTPFKAMWREAKECIYEQDADS 367
Db 306 TDTVAHHLFSTMPHYNAMEATKAIPKILGDYIQFDGTPWYVAMYREAKECIYVSPDREG 365
QY 368 KHKGTYWYH 376
Db 366 DKKGYYWYN 374

RESULT 3
US-11-056-355B-42537
; Sequence 42537, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
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; NAME/KEY: peptide
; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 6444002
US-11-056-355B-75575

Query Match      58.2%; Score 1215; DB 7; Length 377;
Best Local Similarity 55.6%; Pred. No. 1.8e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY      8 RKKDHMDERAFIDPAPFSLDKKAIPAHCPRFSAVSSCVVQDLITFLITYVANTY 67
Db      8 KKSETDTTKRVPCCKPPFSGVGLKKAIPHCPRGISPRISFSLIDIIIIASCFYVATNY 67

QY      68 IPHLPPLVYLAWPVYWFQSCILITGLVWLHECGHHAPESEYOWTDNAVGVFLVHALTLP 127
Db      68 FSLLPQPLSYLAWPLYWACQGVLTGIWIAHECGHAFPSDYQWLDDTDTGLIFHSFLVLP 127

QY      128 YFSWKYSHRKHANTSNLENEEVIPTQSQRTYSTYEFLDNTPEGRILILVIMLTGLFP 187
Db      128 YFSWKYSHRRHSHNTSGTIERDEVFPVKQSAIKWYKY--LNNPLGRIMLTVQFVLGWP 185

QY      188 LYLLTNVSGKKYDRFNNHFDPLSPITFERERTQVALSDLGIVAVPYGKLFVQTGFGQW 247
Db      186 LYLAFFNVSGRPYDGFACHPFPNAPIYNDRELRQIYLSDAGILAVCGLYRYAAAGQMSM 245

QY      248 MCNYGVPVTLGNSFTIIVITLHHTHLSSPHYDSTENWIKGALTITIDRDFGLLAEVHDV 307
Db      246 ICLYGVELLIYVNAFLVLIYLOHTHPSLPHYDSEWMLRGALATVDRDYGILNKVFHNI 305

QY      308 THTVHLHLPPIPHYHAKEASEAIKPILDGYRMIIDRTPPFKAMWREAKECIYIEQDADS 367
Db      306 TDTVAHHLFTSMYPHNAMEAKAIKPILDGYDQDGTIPWYVAMYREAKECIYVEPDREG 365

QY      368 KHKGTWYXH 376
Db      366 DKKGVTWYN 374

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RESULT 5
US-11-056-355B-98547
; Sequence 98547, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98547
; LENGTH: 377
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 13600978
US-11-056-355B-98547

Query Match          58.2%;   Score 1215;   DB 7;   Length 377;
Best Local Similarity 55.6%;   Pred. No. 1.8e-103;
Matches 205;   Conservative 70;   Mismatches 92;   Indels 2;   Gaps 1

QY      8  RMDKDHMDERAPIDDPAPFSLDLKKAIAPACFRRSAAVWSGCVVQDLITITFLLYTVANTY 67
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      8  KKSETDTTKRVCKEKPFPFVGDLKKAIAPHCCKRSIPRSFSLISDIIIASCFYVATNY 67
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      68  IPLHPPLVYLAWPVVYWFQCSCLTGLWVLGHECGHAFSEYQWIDNAVGVFLHSALLTP 127
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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Db	68	PSLLPQPLSYLAWPLYNACQCQCVLTGTGVIWAIEHCCHGHAFFSDYQWLDDTVGLFIHFSFLI	127
Qy	128	YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTGRILILVIMLTGLGPP	187
Db	128	YFSWKYSHRRHSHNTGSLERDEVFPVKQSAIKWYKY--LNNPLGRIMMLTVQFVLGWP	185
Qy	188	LYLLTNVSGKKYDRFTNHFDPLSPITFTRERIRIOVALSDLGIVAVPYGLKFLVQTKFGWV	247
Db	186	LYLAFNVSGRPYDGFACHFFFNAPLYNDRERLQIYLSDAGILAVCFGLYRYAAACQGMAS	245
Qy	248	MCMTGVPVIGLNSFLIIVTYLHHTHLLSPHYDSTEWNNIKGALTITDRDFGLLNRFVHDV	307
Db	246	ICLYGVPLLIYNAFLVLTLYLQHTHPSLPHYDSSDWMRLGALATVDRDYGILNKVFHNI	305
Qy	308	THTHVLHLFPYIPIHYHAKASEAIKPILGDRYMRIDRTFFPKAMWREAKECIYIEODADS	367
Db	306	TDTHVAHHLFSTMPHYNAMEATKAIKPILGDYQDPGTPTVYVAMYREAKECIYVBPDRG	365
Qy	368	KHKGTYYTH 376	
Db	366	DKKGVTYTN 374	
RESULT 6			
US-11-056-355B-109786			
; Sequence 109786, Application US/11056355B			
; Publication No. US20060150283A1			
; GENERAL INFORMATION:			
; APPLICANT: Brover, Vyacheslav			
; APPLICANT: Alexandrov, Nikolai			
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding			
; TITLE OF INVENTION: Polypeptides Encoded Thereby			
; FILE REFERENCE: 2750-1590FUS2			
; CURRENT APPLICATION NUMBER: US/11/056.355B			
; CURRENT FILING DATE: 2005-02-14			
; PRIOR APPLICATION NUMBER: 60/544,190			
; PRIOR FILING DATE: 2004-02-13			
; NUMBER OF SEQ ID NOS: 119966			
; SEQ ID NO 109786			
; LENGTH: 377			
; TYPE: prt			
; ORGANISM: Arabidopsis thaliana			
; FEATURE:			
; NAME/KEY: peptide			
; LOCATION: (1)..(377)			
; OTHER INFORMATION: Ceres Seq. ID no. 13600978			
US-11-056-355B-109786			
Query Match 58.2%; Score 1215; DB 7; Length 377;			
Best Local Similarity 55.6%; Pred. No. 1.8e-103;			
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1			
Qy	8	RMKDHMDERAPIDPAPESLQDLKKAIPAHCFRRSAVWSSCVVODLIITFLTYTANTY	67
Db	8	KKSETDTTKRVPCEKPPFSGDLKKAIPHCFKRSIPRSFSLISDIIASFYIVATNY	67
Qy	68	IPHLPPPLVYLAWPYVFCQSCILTGLWVLGHECHGHAFSEYQWIDNAVGVFLHLSALLTP	127
Db	68	PSLLPQPLSYLAWPLYNACQCQCVLTGTGVIWAIEHCCHGHAFFSDYQWLDDTVGLFIHFSFLI	127
Qy	128	YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTGRILILVIMLTGLGPP	187
Db	128	YFSWKYSHRRHSHNTGSLERDEVFPVKQSAIKWYKY--LNNPLGRIMMLTVQFVLGWP	185
Qy	188	LYLLTNVSGKKYDRFTNHFDPLSPITFTRERIRIOVALSDLGIVAVPYGLKFLVQTKFGWV	247
Db	186	LYLAFNVSGRPYDGFACHFFFNAPLYNDRERLQIYLSDAGILAVCFGLYRYAAACQGMAS	245
Qy	248	MCMTGVPVIGLNSFLIIVTYLHHTHLLSPHYDSTEWNNIKGALTITDRDFGLLNRFVHDV	307
Db	246	ICLYGVPLLIYNAFLVLTLYLQHTHPSLPHYDSSDWMRLGALATVDRDYGILNKVFHNI	305
Qy	308	THTHVLHLFPYIPIHYHAKASEAIKPILGDRYMRIDRTFFPKAMWREAKECIYIEODADS	367

Db 306 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTWPVYAMVREAKECIYVEPDREG 365  
QY 368 KHKGTYYWH 376  
Db 366 DKKGYYWYN 374

RESULT 7  
US-11-058-746-6  
; Sequence 6, Application US/11058746  
; Publication No. US20060101543A1  
; GENERAL INFORMATION:  
; APPLICANT: Somerville, Chris  
; APPLICANT: Broun, Pierre  
; APPLICANT: Van de Loo, Frank  
; APPLICANT: Boddupalli, Sekhar S  
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 56100-5022-12  
; CURRENT APPLICATION NUMBER: US/11/058,746  
; CURRENT FILING DATE: 2005-02-16  
; PRIOR APPLICATION NUMBER: US 08/597,313  
; PRIOR FILING DATE: 1996-02-06  
; PRIOR APPLICATION NUMBER: US 08/530,862  
; PRIOR FILING DATE: 1995-09-20  
; PRIOR APPLICATION NUMBER: US 08/320,982  
; PRIOR FILING DATE: 1994-10-11  
; PRIOR APPLICATION NUMBER: US 08/314,596  
; PRIOR FILING DATE: 1994-09-26  
; PRIOR APPLICATION NUMBER: PCT/US95/11855  
; PRIOR FILING DATE: 1995-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-058-746-6

Query Match 58.2%; Score 1215; DB 7; Length 383;  
Best Local Similarity 55.6%; Pred. No. 1.9e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVVDLIITFLTYVANTY 67  
Db 14 KKSETDTTKRVPCCKPPFSGDLKKAIPPHCFKRSIPRSFSLISDIIIASCFYVATNY 73  
QY 68 IPHLPPLVYLAWPYWFCQSCILTGLWLGHECGHAFSEYQWIDNAVGVLSALLTP 127  
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDVTGLIFHSFLVLP 133  
QY 128 YFSWKYSHRKHANTNSLENEEVIPTQSOLRTYSTYEFLDNTPTGRILILVIMLTGFP 187  
Db 134 YFSWKYSHRRHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQVFLGWP 191  
QY 188 LYLTVNSGKGYDRFTNHFDPSPIFTERERIQVALSDLGIVAVFYGLKPLVQTKGFGW 247  
Db 192 LYLAFNVSGRPYDGFACFPFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGQWASM 251  
QY 248 MCYGVVPGLNSPIVITYLHHTLSSPHYDSTWNNIKGALTITIDRDPGLLNRFVHDV 307  
Db 252 ICLYGVPLLIWNAFLVLTQLHTPSLPHYDSSWDWLRGALATVDRDYGILNKVFHNI 311  
QY 308 THTVHLHLFPYIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIYIEQDADS 367  
Db 312 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTWPVYAMVREAKECIYVEPDREG 371  
QY 368 KHKGTYYWH 376  
Db 372 DKKGYYWYN 380

RESULT 9  
US-11-056-355B-42536  
; Sequence 42536, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966

RESULT 8  
US-11-056-355B-39928  
; Sequence 39928, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 39928  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(383)  
; OTHER INFORMATION: Ceres Seq. ID no. 12370300  
US-11-056-355B-39928

Query Match 58.2%; Score 1215; DB 7; Length 383;  
Best Local Similarity 55.6%; Pred. No. 1.9e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVVDLIITFLTYVANTY 67  
Db 14 KKSETDTTKRVPCCKPPFSGDLKKAIPPHCFKRSIPRSFSLISDIIIASCFYVATNY 73  
QY 68 IPHLPPLVYLAWPYWFCQSCILTGLWLGHECGHAFSEYQWIDNAVGVLSALLTP 127  
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDVTGLIFHSFLVLP 133  
QY 128 YFSWKYSHRKHANTNSLENEEVIPTQSOLRTYSTYEFLDNTPTGRILILVIMLTGFP 187  
Db 134 YFSWKYSHRRHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQVFLGWP 191  
QY 188 LYLTVNSGKGYDRFTNHFDPSPIFTERERIQVALSDLGIVAVFYGLKPLVQTKGFGW 247  
Db 192 LYLAFNVSGRPYDGFACFPFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGQWASM 251  
QY 248 MCYGVVPGLNSPIVITYLHHTLSSPHYDSTWNNIKGALTITIDRDPGLLNRFVHDV 307  
Db 252 ICLYGVPLLIWNAFLVLTQLHTPSLPHYDSSWDWLRGALATVDRDYGILNKVFHNI 311  
QY 308 THTVHLHLFPYIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIYIEQDADS 367  
Db 312 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTWPVYAMVREAKECIYVEPDREG 371  
QY 368 KHKGTYYWH 376  
Db 372 DKKGYYWYN 380

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; SEQ ID NO 42536
; LENGTH: 383
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 12337751
US-11-056-355B-42536

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCFFKRSIPRSFSLIISDIILASCFYVATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLLVP 133

QY 128 YFSWKYSRKHKHAHNTNSLENEEVIIPRTQSQRITSTYEFDLNTPGRILILVIMLTGFP 187
Db 134 YFSWKYSRHRHSHNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFFPNAPYINDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251

QY 248 MCMYGVPIVGLNSFIIVITVYHHTHLSPPHYDSTENWIKGALTTIDRDFGLNRFVHDV 307
Db 252 ICYGVPELLIVNAFLVLTLYLQHTPSLPHYDSSEMDLWLGALATVDRDYGILNKVFHNI 311

QY 308 THTVHLHLFPYIPHYHAKESAIKPILDYRMDIRTPFFKAMWREAKECIYIEQDADS 367
Db 312 TDTHVAHLFSTMPHYNAMEATKAIPILGDYIYQFDGTPWYVAMYREAKECIYVEPDREG 371

QY 368 KHKGTYWYH 376
Db 372 DKKGVTWYN 380

RESULT 11
US-11-056-355B-98546
; Sequence 98546, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98546
; LENGTH: 383
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 13600977
US-11-056-355B-98546

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCFFKRSIPRSFSLIISDIILASCFYVATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLLVP 133

QY 128 YFSWKYSRKHKHAHNTNSLENEEVIIPRTQSQRITSTYEFDLNTPGRILILVIMLTGFP 187
Db 134 YFSWKYSRHRHSHNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFFPNAPYINDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCFFKRSIPRSFSLIISDIILASCFYVATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLLVP 133

QY 128 YFSWKYSRKHKHAHNTNSLENEEVIIPRTQSQRITSTYEFDLNTPGRILILVIMLTGFP 187
Db 134 YFSWKYSRHRHSHNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFFPNAPYINDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCFFKRSIPRSFSLIISDIILASCFYVATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGVFLHSALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLLVP 133

QY 128 YFSWKYSRKHKHAHNTNSLENEEVIIPRTQSQRITSTYEFDLNTPGRILILVIMLTGFP 187
Db 134 YFSWKYSRHRHSHNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFFPNAPYINDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251
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	QY	68	IPHLPPPLVYLAWPVYWFQCSCILITGLWVLGHECGHAFSEYQWIDNAGFVLHSALITP	127
	Db	74	FSLLPQLSYLAWPLYMACQCVLTGIWVIAHECCHAFSDYQWLDDTGVLIHFSPLLVP	133
	QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRSTYSTVEFLDNTPGRIILIVIMLTIGFP	187
	Db	134	YFSWKYSHRRHSHNTGSLSERDEVFVPKQSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP	191
	QY	188	LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQUALSDLGIVAVFYGLKFLVQTGFQGW	247
	Db	192	LylaFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLS DAGILAVCFGLRYAQAQGMSM	251
	QY	248	MCMYGPVIGLNSFIIVITYLHHTHLSSPHYDSTENMWIKGALTITIDRDFGLLRNFHDV	307
	Db	252	ICLYGVPLLIWNAFLVLIYLOHTHPSLPHYDSSEWDNLRGALATVDROYGILNKVFHNI	311
	QY	308	TTHTVLHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEODADS	367
	Db	312	TDTVAHHLFSTMTPHYNAMETNAIKPILGDYYQDGTPTWYVAMYREAKECIYVEPDREG	371
	QY	368	KHKGTYYWH	376
	Db	372	DKKGVTWYN	380
			Search completed: September 22, 2006, 19:59:58	
			Job time : 35 secs	

  

	QY	68	IPHLPPPLVYLAWPVYWFQCSCILITGLWVLGHECGHAFSEYQWIDNAGFVLHSALITP	127
	Db	74	FSLLPQLSYLAWPLYMACQCVLTGIWVIAHECCHAFSDYQWLDDTGVLIHFSPLLVP	133
	QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRSTYSTVEFLDNTPGRIILIVIMLTIGFP	187
	Db	134	YFSWKYSHRRHSHNTGSLSERDEVFVPKQSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP	191
	QY	188	LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQUALSDLGIVAVFYGLKFLVQTGFQGW	247
	Db	192	LylaFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLS DAGILAVCFGLRYAQAQGMSM	251
	QY	248	MCMYGPVIGLNSFIIVITYLHHTHLSSPHYDSTENMWIKGALTITIDRDFGLLRNFHDV	307
	Db	252	ICLYGVPLLIWNAFLVLIYLOHTHPSLPHYDSSEWDNLRGALATVDROYGILNKVFHNI	311
	QY	308	TTHTVLHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEODADS	367
	Db	312	TDTVAHHLFSTMTPHYNAMETNAIKPILGDYYQDGTPTWYVAMYREAKECIYVEPDREG	371
	QY	368	KHKGTYYWH	376
	Db	372	DKKGVTWYN	380
			Search completed: September 22, 2006, 19:59:58	
			Job time : 35 secs	

  

	QY	68	IPHLPPPLVYLAWPVYWFQCSCILITGLWVLGHECGHAFSEYQWIDNAGFVLHSALITP	127
	Db	74	FSLLPQLSYLAWPLYMACQCVLTGIWVIAHECCHAFSDYQWLDDTGVLIHFSPLLVP	133
	QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRSTYSTVEFLDNTPGRIILIVIMLTIGFP	187
	Db	134	YFSWKYSHRRHSHNTGSLSERDEVFVPKQSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP	191
	QY	188	LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQUALSDLGIVAVFYGLKFLVQTGFQGW	247
	Db	192	LylaFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLS DAGILAVCFGLRYAQAQGMSM	251
	QY	248	MCMYGPVIGLNSFIIVITYLHHTHLSSPHYDSTENMWIKGALTITIDRDFGLLRNFHDV	307
	Db	252	ICLYGVPLLIWNAFLVLIYLOHTHPSLPHYDSSEWDNLRGALATVDROYGILNKVFHNI	311
	QY	308	TTHTVLHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEODADS	367
	Db	312	TDTVAHHLFSTMTPHYNAMETNAIKPILGDYYQDGTPTWYVAMYREAKECIYVEPDREG	371
	QY	368	KHKGTYYWH	376
	Db	372	DKKGVTWYN	380
			Search completed: September 22, 2006, 19:59:58	
			Job time : 35 secs	

  

	QY	68	IPHLPPPLVYLAWPVYWFQCSCILITGLWVLGHECGHAFSEYQWIDNAGFVLHSALITP	127
	Db	74	FSLLPQLSYLAWPLYMACQCVLTGIWVIAHECCHAFSDYQWLDDTGVLIHFSPLLVP	133
	QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRSTYSTVEFLDNTPGRIILIVIMLTIGFP	187
	Db	134	YFSWKYSHRRHSHNTGSLSERDEVFVPKQSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP	191
	QY	188	LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQUALSDLGIVAVFYGLKFLVQTGFQGW	247
	Db	192	LylaFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLS DAGILAVCFGLRYAQAQGMSM	251
	QY	248	MCMYGPVIGLNSFIIVITYLHHTHLSSPHYDSTENMWIKGALTITIDRDFGLLRNFHDV	307
	Db	252	ICLYGVPLLIWNAFLVLIYLOHTHPSLPHYDSSEWDNLRGALATVDROYGILNKVFHNI	311
	QY	308	TTHTVLHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEODADS	367
	Db	312	TDTVAHHLFSTMTPHYNAMETNAIKPILGDYYQDGTPTWYVAMYREAKECIYVEPDREG	371
	QY	368	KHKGTYYWH	376
	Db	372	DKKGVTWYN	380
			Search completed: September 22, 2006, 19:59:58	
			Job time : 35 secs	

  

	QY	68	IPHLPPPLVYLAWPVYWFQCSCILITGLWVLGHECGHAFSEYQWIDNAGFVLHSALITP	127
	Db	74	FSLLPQLSYLAWPLYMACQCVLTGIWVIAHECCHAFSDYQWLDDTGVLIHFSPLLVP	133
	QY	128	YFSWKYSHRKHANTNSLENEEVYIPRTQSOLRSTYSTVEFLDNTPGRIILIVIMLTIGFP	187
	Db	134	YFSWKYSHRRHSHNTGSLSERDEVFVPKQSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP	191
	QY	188	LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQUALSDLGIVAVFYGLKFLVQTGFQGW	247
	Db	192	LylaFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLS DAGILAVCFGLRYAQAQGMSM	251
	QY	248	MCMYGPVIGLNSFIIVITYLHHTHLSSPHYDSTENMWIKGALTITIDRDFGLLRNFHDV	307
	Db	252	ICLYGVPLLIWNAFLVLIYLOHTHPSLPHYDSSEWDNLRGALATVDROYGILNKVFHNI	311
	QY	308	TTHTVLHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEODADS	367
	Db	312	TDTVAHHLFSTMTPHYNAMETNAIKPILGDYYQDGTPTWYVAMYREAKECIYVEPDREG	371
	QY	368	KHKGTYYWH	376
	Db	372	DKKGVTWYN	

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: September 22, 2006, 19:38:36 ; Search time 42 Seconds  
(without alignments)  
865.951 Million cell updates/sec  
Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDRMKDHMDERAPI.....IYIEQDADSKHGTYWYHKM 378  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES					Query		Description	
Result No.	Score	Match	Length	ID	*			
1	1271	60.9	383	T10480	Deltal2 fatty acid			
2	1240	59.4	382	T15042	omega-6 fatty acid			
3	1234	59.2	383	T07688	omega-6 desaturase			
4	1226	58.8	383	T10789	omega-6 desaturase			
5	1214.5	58.2	385	T09880	Deltal2 fatty acid			
6	1203	57.7	378	T14269	oleate 12-hydroxyl			
7	1192	57.1	387	T09839	fungal elicitor-in			
8	1176	56.4	383	T15043	omega-6 desaturase			
9	1170.5	56.1	387	T07687	omega-6 fatty acid			
10	1090	52.3	333	T07009	stearoyl-CoA 9-des			
11	907.5	43.5	376	JC7871	omega-3 fatty acid			
12	640	30.7	359	AG2005	omega-3 fatty acid			
13	638	30.6	441	T03029	omega-3 fatty acid			
14	634	30.4	431	T07685	omega-3 fatty acid			
15	612.5	29.4	438	T15039	omega-3 fatty acid			
16	611.5	29.3	460	T10063	omega-3 fatty acid			
17	603	28.9	398	T01696	omega-3 fatty acid			
18	602.5	28.9	453	1 JQ2339	omega-3 fatty acid			
19	601	28.8	379	JC3555	omega-3 fatty acid			
20	597.5	28.6	386	1 JQ2335	omega-3 fatty acid			
21	594.5	28.5	381	2 T03923	probable omega-3 f			
22	594	28.5	443	2 T01697	omega-3 fatty acid			
23	593.5	28.5	446	1 JQ2336	omega-3 fatty acid			
24	588.5	28.2	377	1 JQ2337	omega-3 fatty acid			
25	587.5	28.2	418	2 JC7872	stearoyl-CoA 9-des			
26	585	28.0	380	2 T10898	probable omega-3 f			
27	583	27.9	404	2 PQ0812	omega-3 fatty acid			
28	579.5	27.8	383	1 A44227	omega-3 fatty acid			
29	578.5	27.7	380	2 JQ2338	omega-3 fatty acid			

RESULT 1  
T10480  
Deltal2 fatty acid desaturase (EC 1.14.99.-) [imported] - Commerson's wild potato  
C:Species: Solanum commersonii (Commerson's wild potato)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10480  
R:Consiglio, F.; Amatruda, M.R.; Leone, A.; Costa, A.; Grillo, S.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z17044  
A:Accession: T10480  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-383 <CON>  
A:Cross-references: UNIPROT:Q41305; UNIPARC:UPI0000033AA3; EMBL:X92847; NID:gl054842; PII  
A:Experimental source: clone ScDes D111  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis  
Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 2.7e-99;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;

QY	16	ERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVVDLIITFLTYVANTYIPHLPPPL	75
DB	22	QKVPTSKPFTVGDIKKAIPHCQFSLRSYVVDLILVSIMYVANTYFHLPPSY	81
QY	76	VYLAWPVVWFOQCILTGLWVLGHEGHHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSH	135
DB	82	CYIAWPIYWCQGCVCCTGIWVNAHECGHAFSDYQWDDTVGLILHSALLVPYFSWKYSH	141
QY	136	RKHANTNSLENEEYVYIPRTQSOLATYTYEFLDNTGRILILVIMLTGLGFLYLLTNVS	195
DB	142	RRHNSNTGSLREDFVFPKPSQLGWYSKY--LNNPPGRVLSLTITLTUGWPLYLAFNVS	199
QY	196	GKKYDRFTNHDFPLSPIFTERERIOVALSDLGIVAFYGLKFLVOTKFGWVMCMYGVFV	255
DB	200	GRPYDRFACHYDPYGPYNNRRLQIFISDAGVLGVCYLLYRIALVKGLAWLCVYGVPL	259
QY	256	IGLNSFIIVTYLHHTLSSPHYDSTEWNIKALTITDRDGLNLRVFDVTHVHLHH	315
DB	260	LVVNGFLVITLQHTPLSPHYDSTEDWLKALATCDRDYGVNLKVPFNHITDTHVHH	319
QY	316	LPFYPHYHAKESAIKPIGLDYRMIDRTPFKAMWEAKECIYEQDADSKHGTYWY	375
DB	320	LFTMPHYNAMEATKAVKPLLDGYQFDGTPYIKEMWEAKECLYVEKDESSQGGKGFVWY	379

RESULT 2  
T15042  
omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley  
C:Species: Petroselinum crispum (parsley)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

Query Match	58.8%	Score 1226;	DB 2;	Length 383;
Best Local Similarity	56.9%	Pred. No. 1.7e-95;		
Matches 205;	Conservative 72;	Mismatches 81;	Indels 2;	Gaps 1
Qy	16	ERAPIDPAPPSLDLKKAI	PAHCPRRS	AVMSCVVQDLIIITFLTYTVA
				NIPIHLPPPL 75
Db	22	KRVYSKPPFPTLSEIKAI	PHCFQSRVLSRFSYLLYDFILASLFYHVA	TNFPNLPQAL 81
Qy	76	VYLAWPVWFQSCILITGL	VLWLGHC	GHAFSEYQWIDNAVGVFLH
				SALLTYFWSKYSH 135
Db	82	SNVAPLYWMOGCLITGV	WIAHECGHAFSDYQMLDDT	VGLILHSSLVYPFWSKYSH 141
Qy	136	RKHANTNSLSENVYIPRT	OSQURTYSTYBFLDNT	PGORILLVIMLTGLGFP
				LYLLTNVS 195
Db	142	RRHHSNTGSLRDEVFV	PKKSGSLRWAAKH--FNNP	PGRFSLTITQLTLGWPLYLAFNVA 1999
Qy	196	GKKYDRFTNHDPDLSPI	PTERRERIOVALSDLGIVAFYGL	KFLVOTKGGWVMCMVGPV 255
Db	200	GRPDRFACHDPPGPIES	DRERLQIYISDAGVLAVAYAL	YELVLAKGVWISVYGVPL 259
Qy	256	IGLNSFIIVTYLHHHTL	SSPHYDSTENWIKGALTIT	IDRDPGLGNRVPHDVTHTVLHH 315
Db	260	LVVNAFLWMIYTLQHTP	SLPHYDSEDMWRGALSTVD	RDRGIINKVPHNITDTHVAHH 319

**A; Experimental source: Strain Mammoth**

QY 196 GKKYDRFTNHFDP LSP IFTERERI QVALSDLGIVAFYGLKFLVQT KGF GWMCMGVGPV 25

Ov 196 GK KYDRETN

A; Experimental source: strain mammoth

1960

Qv 196 GKVVNRETNHEDPI.SPIETERPERTOVAL.SDI.GTIVAFYGI.KET.VOTKGEGW

196 GKKNRPETNTHEDPI.SPTETTERPERTOVALSDI.GTVAVFYGI.KET.VOTKGEFGWMCMYGVPV 255

Db 204 GRPDRFACHYDGPISERERQIYADIAGIFATFVLVQATMAKGLAWMRIYGVPL 263  
Qy 256 IGLNSFIIVITLHHTLSSPHYDSTENWIKGALTITDRDFGLNRRVFDHVTHTVLHH 315  
Db 264 LIVNCFVMTYLTQHTPAIPRYGSSEWDLRGAVTVDRDYGVLNVKFHNIADTHVAH 323  
Qy 316 LPPYIPHYHAKASEAIKPIIGDYRMDIRTPFFKAMWREAKECIYIIBODADSKHGTYWY 375  
Db 324 LFATVPHYHAEATKAIPKINGEYRVDTGTFYKALWREAKECLFVBPDEGAPTQGVFWY 383

RESULT 8  
T15043  
C:Species: Petroselinum crispum (parsley)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T15043  
R:Kirsch, C.; Hahlbrock, K.; Somssich, I.E.  
Plant Physiol. 115, 283-289, 1997  
A:Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desat  
A:Reference number: Z18274; MUID:97451781; PMID:9306702  
A:Accession: T15043  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-383 <KIR>  
A:Cross-references: UNIPROT:O24472; UNIPARC:UPI00000A7AA9; EMBL:U86374; NID:92501791; PI  
C:Genetics:  
A:Gene: ELI12  
C:Superfamily: fatty acid (acyl-CoA) desaturase

Query Match 56.4%; Score 1176; DB 2; Length 383;  
Best Local Similarity 54.5%; Pred. No. 2.7e-91;  
Matches 205; Conservative 74; Mismatches 93; Indels 4; Gaps 3;  
Qy 1 MSDSDVDRMKDHMDERAPIDPAPSLDLKKAIPAHCFRPSAVWSSCYVVDLIITPLL 60  
Db 7 MSDPPSGKKTAAEALKRAPHBKPPPTIGDLKKAIPAHCFQKSLVTSFYLLIQDLFMAVAL 66  
Qy 61 YTVANTYT-PHLPPLVYLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFV 119  
Db 67 FVATNYIDQYLPFPNVMAAYIATVQCVLTGAWVVGHECDHDAFNNYINDLVGLV 126  
Qy 120 LHSALLTPYFNKSHRKHANTNSLENEEVIPTQSQLRTYSTYEFLDNTPGRILLV 179  
Db 127 VHSLLVPYFNGKISHRRHANTQSLNDEVVPRFKSNIRNY--YKLLNPPGKRVLYWL 184  
Qy 180 IMLTLGFPYLLTNVSGKKYDRFTNHPDPLSPIETERERIQVALSDLGIVAFYGLKFLV 239  
Db 185 TTLTGFPYLLMNFVSGHKYERWTSHYDPHSPLYSDRERKEIIVSDIALLAVIYDLYQLV 244  
Qy 240 QTKGFGWCMYGVPIVGLNSPIIIVITLHHTLSSPHYDSTENWIKGALTITDRDFGL 299  
Db 245 LAKGFAWFCVYGGPLLVNGWFLVYTLNHTHPSLPYDSTENWDLRGALCTDVRDYG 304  
Qy 300 LNRVPHDVTHTVLHLLFPYIPHYHAKASEAIKPIIGDYRMDIRTPFFKAMWREAKECI 359  
Db 305 LNKVPHNVCNAHVCHHIFSMIPHYHGLESTEAMKPILGEEYQYDGTPTLKAMWREMKCI 364  
Qy 360 YIEQDADSKHGKTYWY 375  
Db 365 YVEKD-EGETKGVYWY 379

RESULT 9  
T07687  
omega-6 desaturase FAD2-1, microsomal - soybean  
C:Species: Glycine max (soybean)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07687  
R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.  
Plant Physiol. 110, 311-319, 1996  
A:Title: Developmental and growth temperature regulation of two different microsomal om

A:Reference number: Z16095; MUID:96151506; PMID:8587990  
A:Accession: T07687  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-387 <HEP>  
A:Cross-references: UNIPROT:P48630; UNIPARC:UPI0000033AA4; EMBL:L43920; NID:9904151; PID  
A:Experimental source: seed  
C:Genetics:  
A:Gene: FAD2-1  
C:Function:  
A:Description: involved in production of polyunsaturated lipids; plays a major role in c  
A:Note: strongly expressed in developing seeds  
C:Superfamily: fatty acid (acyl-CoA) desaturase

Query Match 56.1%; Score 1170.5; DB 2; Length 387;  
Best Local Similarity 54.0%; Pred. No. 7.9e-91;  
Matches 194; Conservative 71; Mismatches 91; Indels 3; Gaps 2;  
Qy 17 RAPIDPAPFSLDLKKAIPAHCFRPSAVWSSCYVVDLIITFLLYTVANTVYIHLPPPLV 76  
Db 28 RVNTEKPPFTVGQKKAIPHCFQRSULTSFYVYVDLSFAFIY-IATTFHLLPOFSS 86  
Qy 77 YLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFVLHLSALLTPYFSWKYSHR 136  
Db 87 LIAPIYVVLQGCLLTGVWVIAHECGHAFSKYQWVDVVGTLTSHSTLLVPYFSWKISHR 146  
Qy 137 KHANTNSLENEEVIPTQSQLRTYSTYEFLDNTPGRILLVIMLTGLGPLYLLTNVSG 196  
Db 147 RHHSNTGSLDRDEVFVPKPKSKAWMFSKY--LANNPLGRAVSLVTLTIGWPMYLAFNVS 204  
Qy 197 KYDRFTNHPDPLSPIETERERIQVALSDLGIVAFYGLKFLVQTKGFGWCMYGVYVPI 256  
Db 205 RPYDSPASHHPYAPIYSNRERLIIVSDVALPSVTSLYRVATLKLGLVLLCYGVPLL 264  
Qy 257 GLNSFIIVITLHHTLSSPHYDSTENWIKGALTITDRDFGLNRRVFDHVTHTVLHLL 316  
Db 265 IVNGFLVITLYLQHTFALPHYDSSEWDLKALATMDRDYGLNKFHHITDTHVAHL 324  
Qy 317 PPIYIPHYHAKASEAIKPIIGDYRMDIRTPFFKAMWREAKECIYIEQADSKHGKTYWY 375  
Db 325 FSTMPHYHAEATNAIKPILGEEYQYDGTPTFYKALWREARECLYVBPDEGTSEKGVYWY 383

RESULT 10  
T07009  
omega-6 fatty acid desaturase (EC 1.14.99.-) defense-related - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T07009  
R:Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.  
Mol. Plant Microbe Interact. 9, 409-415, 1996  
A:Title: Characterization of defense-related genes ectopically expressed in viroid-infect  
A:Reference number: Z15859; MUID:96252900; PMID:8672818  
A:Accession: T07009  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-333 <GAD>  
A:Cross-references: UNIPROT:Q43500; UNIPARC:UPI00000A4D15; EMBL:X94944; NID:g1161567; PI  
A:Experimental source: cultivar Rutgers; leaf  
C:Genetics:  
A:Gene: cev119  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
C:Keywords: oxidoreductase

Query Match 52.3%; Score 1090; DB 2; Length 333;  
Best Local Similarity 52.5%; Pred. No. 3.9e-84;  
Matches 189; Conservative 55; Mismatches 64; Indels 52; Gaps 3;  
Qy 16 ERAIDPAPFSLDLKKAIPAHCFRPSAVWSSCYVVDLIITFLLYTVANTVYIHLPPPL 75  
Db 22 ERVPSSKPPFTLGDVYKKAIPHCFQRSULTSFYVYVDLSFAFIY-IATTFHLLPOFSS 81  
Qy 76 VYLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFVLHLSALLTPYFSWKYSH 135



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Db 82 RYVAVTYIAQCVCVTGIVWIGHECGHGFSDYQWVDDIVGLILHSALLTFYFAWKSH 141
Qy 136 RKHHANTNSLENEEVIPRTOSQLRTYSTYFELNDTPGRILILVIMLTGLGFLYLLTNVS 195
Db 142 RRHHANTNSLENEEIVIPRLKSLR----- 166
Qy 196 GKXYDRFTNHPDPLSPFITERERIOVALSDLGIVAVFYGLKFLVQPKFGWCMVGVV 255
Db 167 GKXYDRFACHYPSPISYNNRRLQIYSDVGVIATYLLYRVTLTQ----- 213
Qy 256 IGLNSFIIVTYLHTLSSPHYDSFENWIKGALTITDRDGLNRFVHDVTHTVLHH 315
Db 214 -GLAGEIVLITLMTHTSLSPHYDSSEWDLRGALATVDRDYGLANKVPHNVTDTHVLHH 272
Qy 316 LPYIPPHYHAKASEAIKPIGLGYRMDTRTPPFKAMWREAKECIYFEQDADSKHGTYWY 375
Db 273 IFSYISHYHAMEAKKAIPKELGEEYKYDDTPILKAMWRTKECIFVEKOKD---KGVYVY 329

RESULT 11
JC7871
stearyl-CoA 9-desaturase (EC 1.14.19.1), PAD2 - Chlorella vulgaris
N:Alternate names: acyl-CoA desaturase; delta12 stearoyl-CoA desaturase; delta9-desaturase
C:Species: Chlorella vulgaris
C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C:Accession: JC7871
R:Suiga, K.; Honjoh, K.; Furuwa, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.;
BioSci. Biotechnol. Biochem. 66, 1314-1327, 2002
A:Title: Two low-temperature-inducible Chlorella genes for delta12 and omega-3 fatty acid
s cerevisiae, and expression of omega-3 fad in Nicotiana tabacum.
A:Reference number: JC7871; MUID:22152188; PMID:12162554
A:Accession: JC7871
A:Molecule type: mRNA
A:Residues: 1-376 <SUG>
A:Cross-references: UNIPROT:Q8W314; UNIPARC:UPI00000A8B54; DDBJ:AB075526
C:Comment: This enzyme is involved in low temperature adaptation, and is also involved in
C:Genetics:
A:Gene: fad2
C:Superfamily: fatty acid (acyl-CoA) desaturase
C:Keywords: oxidoreductase

Query Match 43.5%; Score 907.5; DB 2; Length 376;
Best Local Similarity 45.8%; Pred. No. 1e-68;
Matches 168; Conservative 76; Mismatches 112; Indels 11; Gaps 8;

Qy 17 RAPIDPAP-FSLSDLKKAIPAHCFRRSAVSSCVVQDLIITFLTYVANTYIPHLPPPL 75
Db 15 RQPVNTKPAFSTVTLRKAIPAHCFRRSAVSSCVVQDLIITFLTYVANTYIPHLPPPL 73
Qy 76 V--YLA-WPVYFQCSCILTLGLVHGHECHHAFSEYQWIDNAGVFLHSALITPYFSWK 132
Db 74 AVRWLALNPAYWYLAGAVATGIVIAHECHQHAFSDYQAVNDGVGLVLSLLLVPIYSWK 133
Qy 133 YSHRKHANTNSLENEEVIPRTOSQLRTYSTYFELNDTPGRILILVIMLTGLGFLYLLT 192
Db 134 HSHRRHNTGNVNDKDEVPVPTREVS--DKWELEQAMPRLVKLFIITLGLWPLYLAF 191
Qy 193 NVSGKKYDR-FTNHPDPLSPFITERERIOVALSDLGIVAVFYGLKFLVQPKFGWCMV 251
Db 192 NVASREYKSNWNHFDWSPISFKRELVEVAVSDAALVLCGLRQLAASFGWMLVKTW 251
Qy 252 GYPVIGLNSFIIVTYLHTLSSPHYDSFENWIKGALTITDRDGLNRFVHDVTHTVH 310
Db 252 LVPYLNVNFWLVTITLQWLSHPLPHYGEDWDLRGALTVDYDGLNLSLHHIADT 311
Qy 311 HVLHLFPYIPHYHAKASEAIKPIGLGYRMDTRTPPFKAMWREAKECIYFEQDADSKHK 370
Db 312 HVAHLFSPQPHYHAQENTALKPVLDYRSRPLQLQAIWQDFSCRYVADTFG--D 369

Qy 371 GTYWHK 377
Db 370 GVLWFK 376
```

## RESULT 12

```
AG2005
omega-3 fatty acid desaturase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C:Accession: AG2005
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
R.; Kaneko, T.; Nakamura, Y.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
Nakazaki, N.; Shimpo, S. 2001
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KUR>
A:Cross-references: UNIPROT:Q8YWL1; UNIPARC:UPI00000CE141; GB:BA000019; PIDN:BAB77963.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1597
C:Superfamily: fatty acid (acyl-CoA) desaturase

Query Match 30.7%; Score 640; DB 2; Length 359;
Best Local Similarity 36.1%; Pred. No. 3.2e-46;
Matches 122; Conservative 74; Mismatches 122; Indels 20; Gaps 6;

Qy 24 PFSLDLKAIPAHCFRRSAVSSCVVQDLIITFLTYVANTYIPHLPPPLVYLAWPVY 83
Db 24 PFTLDLKAIPAHCFRRSAVSSCVVQDLIITFLTYVANTYIPHLPPPLVYLAWPVY 83
Qy 84 WFCQSCILTLGLVHGHECHHAFSEYQWIDNAGVFLHSALITPYFSWKYSHRKHANTN 143
Db 77 WLIOQTMFWALFVGHGCHQHQSFKHNLNDLGLHTHTFLVYPVHGWRISHRTHKNTG 136
Qy 144 SLENEEVIPRTOSQLRTYSTYFELNDTPGRILILVIMLTGLGFLYLLTNVSGKKYDR 203
Db 137 NIDNDESWYPTQSQVKEMP---LQKIGIYVVF---LAYPVYLFKRSNPK---G 184
Qy 204 NHFDPLSPFITERERIOVALSDLGIVAVFYGLKFLVQPKFGWCMVGVVIGLSFII 263
Db 185 SHFLPSSSLFKPSEKWDVITSTVLSWCMVGLGFLTYQGMWMLLKYAAPYIVFVILWD 244
Qy 264 VTYLHTLSSPHYDSFENWIKGALTITDRDGLNRFVHDVTHTVLHLFPYIPHY 323
Db 245 LVTFLLHTEADLPWYRGEDWTLKGAISSIDRYGLVNHIIHDI-GTHVAHIFLNI 303
Qy 324 HAKEASEAIKPIGLGYRMDTRTPPFKAMWREAKECIYI 361
Db 304 NLKATEAIKPVWGEYRKSEBPIWKSLLWRSVCVSHFV 341

RESULT 13
T03029
omega-3 fatty acid desaturase (EC 1.14.99.-) PAD7 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03029
R:Hamada, T.; Nishuchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
Plant Cell Physiol. 37, 606-611, 1996
A:Title: CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid
A:Reference number: Z14828; MUID:96416425; PMID:8819308
A:Accession: T03029
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-441 <HAM>
A:Cross-references: UNIPROT:P93350; UNIPARC:UPI00000A5D90; EMBL:D79979; NID:g1694624; PII
A:Experimental source: cultivar SR1
C:Genetics:
A:Gene: PAD7
C:Superfamily: fatty acid (acyl-CoA) desaturase
C:Keywords: oxidoreductase
```

Query Match 30.6%; Score 638; DB 2; Length 441;  
Best Local Similarity 37.9%; Pred. No. 5.9e-46;  
Matches 136; Conservative 62; Mismatches 129; Indels 32; Gaps 10;

QY 19 PIDAPPSSLDKKAIPAHCRRSAVWSSCYVQDLITFLTYTANTYIYIPLPPLVYL 78  
DB 89 PGAPPPFKLSIDKKAIPKHCWVKNPKWSYVVRDVAIVFGL-AAAAAYFNN-----WV 141  
QY 79 AWPVYWFQSCILTGLWVLCGCHHAFSEYQWIDNAVGVFLHLSALLTPYFSWKYSHRKH 138  
DB 142 WPLVYMPAQSMFVALFVLGHDCHGSGFSNNHKLNSVGVHILHSSILVPYHGWRISHRTH 201  
QY 139 HANTNSLENEEVIYPTQSLRTYSTYFPLDTPGRIILVIMLTGLFPLYLITNSGKK 198  
DB 202 HQNHGHVNDSEWHPIPE-----KIYNSLDLTKKLRFTLPPLLAYPFLYLGWSRSPGKK 255  
QY 199 YDRFTNHPDPSIPFTEERRERIOVALSDL--GIVAVFYGLKFLVQTKGFGWCMVGVVPV 255  
DB 256 ----GSHFDPPNSDLFVPSKKVDVMTSLCWTAMALLVGLSFVM---GPFQVLKLYGIPY 308  
QY 256 IGLNSFIIVTYLHHTHLS--PHYDSTENWIKGALTITDRDGLLNRPVHDVTHVL 313  
DB 309 WGFVWMLDVTYLLHHGHDDKLPWYRGESYLRGLTTLDRDYGWINNIHDI-GTHVI 367  
QY 314 HHLFPYIHYHAKESAIAKILGDY-----RMIDRTPF--KAMWREAKECIYIEQDAD 366  
DB 368 HHLFPQIHYHLVEATEAAKPVLGKYYKEPKSGPLPFLYLGVLKSMQDHYVSDTGD 426

RESULT 14  
T07685  
omega-3 fatty acid desaturase (EC 1.14.99.-) - potato  
N/Alternate names: w-3 desaturase  
C/Species: Solanum tuberosum (potato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07685  
R/Leon, J.  
submitted to the EMBL Data Library, August 1998  
A/Reference number: Z16092  
A/Accession: T07685  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-431 <LEO>  
A/Cross-references: UNIPROT:082068; UNIPARC:UPI000009E6DD; EMBL:AJ007739; PIDN:CAA07638.  
A/Experimental source: cv. Desiree  
C/Function:  
A/Pathway: fatty acid biosynthesis  
A/Superfamily: fatty acid (acyl-CoA) desaturase  
C/Keywords: oxidoreductase

Query Match 30.4%; Score 634; DB 2; Length 431;  
Best Local Similarity 38.9%; Pred. No. 1.3e-45;  
Matches 132; Conservative 60; Mismatches 121; Indels 26; Gaps 9;

QY 6 DRRMKDHMDERAPIDPAPPSLDKKAIPAHCRRSAVWSSCYVQDLITFLTYTAN 65  
DB 66 EBEQTNNGDEPDGAPPKLSIDKKAIPKHCWKNPKWTSMSYVVRDVAIVFGL-AAAA 124  
QY 66 TYIPLPPLVYLAWPVYWFQSCILTGLWVLCGCHHAFSEYQWIDNAVGVFLHLSALL 125  
DB 125 AYFNN-----WLVWPLYWFAQSMFVALFVLGHDCHGSGFSNNHKLNSVAGHILHSSIL 178  
QY 126 TPYFSWKYSHRKHANTNSLENEEVIYPTQSLRTYSTYFPLDTPGRIILVIMLTIG 185  
DB 179 VPYHGMRIISHRTHQNHGHVNDSEWHPIPE-----KLYNSLDDITKKFRFTLPPLLA 232  
QY 186 PLYLTLTVNSGKKYDRFTNHPDPLSPIFTEERRERIOVALSDL--GIVAVFYGLKFLVQTK 242  
DB 233 YPFLYLGWSRSPGKK-----GSHFDPPNSDLFVASEKKDVITSTVCWTAMALLVGLSFVM--- 285  
QY 243 GFGWVMCMYGVPIGLNSFIIVTYL-HHTHLS--PHYDSTENWIKGALTITDRDGLL 300

DB 286 GPLQVLKLYGIPYWGFMWMLDIVTLHHGHEDKVPWYRGESYLRGLTTLDRDYGWI 345  
QY 301 NRVPDVTHTVHLHLPPYPHYHAKESAIAKILGDY 339  
DB 346 NNIHDI-GTHVIHLLFPQIHYHLVEATEAAKPVLGKY 383

RESULT 15  
T15039  
omega-3 fatty acid desaturase (EC 1.14.99.-), chloroplast - parsley  
C/Species: Petroselinum crispum (parsley)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: T15039  
R/Kirsch, C.; Takamiya-Wik, M.; Reinold, S.; Hahlbrock, K.; Somssich, I.E.  
Proc. Natl. Acad. Sci. U.S.A. 94, 2079-2084, 1997  
A/Title: Rapid, transient, and highly localized induction of plastidial omega-3 fatty ac  
A/Reference number: Z18273; MUID:97203190; PMID:9050908  
A/Accession: T15039  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-438 <KIR>  
A/Cross-references: UNIPROT:P93452; UNIPARC:UPI00000A57CA; EMBL:U75745; NID:G1786065; PII  
C/Genetics:  
A/Genome: nuclear  
C/Function:  
A/Pathway: fatty acid biosynthesis  
A/Note: involved in pathogen defense response  
C/Superfamily: fatty acid (acyl-CoA) desaturase  
C/Keywords: chloroplast; oxidoreductase

Query Match 29.4%; Score 612.5; DB 2; Length 438;  
Best Local Similarity 35.1%; Pred. No. 8.2e-44;  
Matches 129; Conservative 70; Mismatches 133; Indels 35; Gaps 11;

QY 14 MDERAPIDPA---PFSLSDLKKAIPAHCRRSAVWSSCYVQDLITFLTYTANTYIPH 70  
DB 78 VEENEFDPGAAPPKLSIDVRAAIPKHCWVKDPVRSMSYLRDLVIVFGL-AVAASFVN 136  
QY 71 LPPPLVYLAWPVYWFQSCILTGLWVLCGCHHAFSEYQWIDNAVGVFLHLSALLTPYPS 130  
DB 137 -----WAVWPLYWIAQGMFVALFVLGHDCHGSGFSNDKLSNVGVHILHSSILVPYHG 190  
QY 131 WKYSHRKHANTNSLENEEVIYPTQSLRTYSTYFPLDTPGRIILVIMLTGLFPYLYL 190  
DB 191 WRISHRTHQNHGHVNDSEWHPISE-----KLFNSLDDLTFRKFTLPFPLMAYPFL 244  
QY 191 LTNVSGKKYDRFTNHPDPLSPIFTEERRERIOVALSDL--GIVAVFYGLKFLVQTKGFW 247  
DB 245 WGRSPGKK---GSHYDPPSDFVPNERKDVITSTVCWTAMALLVGLNFVM---GPVKM 297  
QY 248 MCMYGVPIGLNSFIIVTYLHHTHLS--PHYDSTENWIKGALTITDRDGLLNRPVH 305  
DB 298 LMLYGIPIYWIWVWMLDFVYLLHHGHDDKLPWYRGKWSYLRGGLTTLDRDYGWINNIH 357  
QY 306 DVTHVHLHLFPYIHYHAKESAIAKILGDY----RMIDRTPF--FKAMWREAKECI 359  
DB 358 DI-GTHVVHLLFPQIHYHLVEATEAAKPVGKYREPKSGPVPFHLATLWKSFKKH 416  
QY 360 YIEQDAD 366  
DB 417 FVSDTGD 423

Search completed: September 22, 2006, 19:44:07  
Job time : 43 secs

GenCore version 5.1.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:35:06 ; Search time 300 Seconds  
(without alignments)  
1165.520 Million cell updates/sec

Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDDRMKDHMDERAPI.....IYIEQDADSKHGTYHYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2086	100.0	378	2 Q6S9E1 STOLA	Q6S9E1 stokesia la
2	1537.5	73.7	377	2 Q7XA13 HELAN	Q7XA13 helianthus
3	1523.5	73.0	377	2 Q9SGG2 CALOF	Q9SGG2 calendula o
4	1493	71.6	374	2 Q65771 CREPIS	Q65771 crepis pala
5	1424.5	68.3	375	1 FAD12 CREAL	Q81931 crepis alpi
6	1410	67.6	326	2 Q7XA09 9ASTR	Q7XA09 dimorphothe
7	1369	65.6	326	2 Q7XA08 9ASTR	Q7XA08 helichrysum
8	1351	64.8	326	2 Q7XA10 RUDHI	Q7XA10 rudbeckia h
9	1290.5	61.9	383	2 Q9SP28 VERGA	Q9SP28 vernonia ga
10	1284.5	61.6	383	2 Q9SP29 VERGA	Q9SP29 vernonia ga
11	1279	61.3	383	2 Q82729 BOROF	Q82729 borago offi
12	1274	61.1	383	2 Q6DMQ8 TOBAC	Q6DMQ8 nicotiana t
13	1274	61.1	383	2 Q2VG85 9ROSI	Q2VG85 jatrophia c
14	1271	60.9	383	2 Q41305 SOLCO	Q41305 solanum com
15	1268.5	60.8	379	2 Q65772 9ASTR	Q65772 crepis pala
16	1265	60.6	367	2 Q84UB7 PUNGR	Q84UB7 punica gran
17	1264	60.6	383	2 Q8GZC3 VERFO	Q8GZC3 vernicia fo
18	1261	60.5	383	2 Q5S3X7 TROMA	Q5S3X7 tropaeolum
19	1260	60.4	382	2 Q8H943 SPIOL	Q8H943 spinacia ol
20	1260	60.4	383	2 Q461Q1 HEVERA	Q461Q1 hevea bras
21	1260	60.4	383	2 Q4QWZ0 OLEEU	Q4QWZ0 olea europa
22	1258	60.3	383	2 Q9LL17 SESIN	Q9LL17 sesamum ind
23	1255.5	60.2	382	2 Q8W2E9 HELAN	Q8W2E9 helianthus
24	1255	60.2	387	2 Q84VT2 PUNGR	Q84VT2 punica gran
25	1252.5	60.0	382	2 Q8H2C3 PERAE	Q8H2C3 persea amer
26	1250	59.9	383	2 Q5FB99 SOVEN	Q5FB99 glycine max
27	1250	59.9	383	2 Q6QDM6 CUCPE	Q6QDM6 cucurbita p
28	1242.5	59.6	383	2 Q9AT72 CALOF	Q9AT72 calendula o
29	1240	59.4	378	2 Q38JF7 LINUS	Q38JF7 linum usita
30	1240	59.4	382	2 Q24471 PETCR	Q24471 petroselinu
31	1239	59.4	383	2 Q8W2F0 HELAN	Q8W2F0 helianthus

32	1238	59.3	383	2 Q8GVC9 OLEEU	Q8GVC9 olea europa
33	1234	59.2	383	1 FDGE2 SOVEN	P48631 glycine max
34	1230.5	59.0	346	2 O81364 PRUAR	O81364 prunus arme
35	1226	58.8	383	2 O23956 GOSHI	O23956 gossypium h
36	1219.5	58.5	384	2 Q8W2B9 GOSHI	Q8W2B9 gossypium h
37	1216.5	58.3	384	2 Q9ZP12 9BRAS	Q9ZP12 brassica ca
38	1216	58.3	379	2 Q4FNJ0 ARAHY	Q4FNJ0 arachis hyp
39	1216	58.3	379	2 Q9LKK5 9FABA	Q9LKK5 arachis dur
40	1215	58.2	383	1 FAD6E ARATH	P46313 arabidopsis
41	1214.5	58.2	385	2 O23955 GOSHI	O23955 gossypium h
42	1214	58.2	379	2 O22628 ARAHY	O22628 arachis hyp
43	1210.5	58.0	384	2 O8LPE8 BRACM	O8LPE8 brassica ca
44	1210	58.0	379	2 Q4UL26 ARAHY	Q4UL26 arachis hyp
45	1209	58.0	384	2 Q9FV88 PETCR	Q9FV88 petroselinu

## ALIGNMENTS

RESULT 1  
Q6S9E1 STOLA PRELIMINARY; PRT; 378 AA.  
AC Q6S9E1;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DE Delta 12 fatty acid epoxigenase.  
OS Stokesia laevis (Stokes' aster).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
OC Vernoniaeae; Stokesia.  
OX NCBI\_TaxID=13696;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RA Hatanaka T., Hildebrand D.F.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
-----  
CC EMBL; AY462108; AAR23815.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016717; P:oxidoreductase activity, acting on paired d. .; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
DR InterPro; IPR005804; FA\_desat.  
DR InterPro; IPR010257; FA\_desat\_sub.  
DR Pfam; PF00487; FA\_desaturase; 1.  
DR PIRSP; PIRSF000347; FA\_acyl-CoA\_des; 1.  
DR ProDom; PD001081; FA\_desat\_sub; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 378 AA; 44164 MW; 4DE2346FDB19BE3A CRC64;

Query Match					100.0%; Score 2086; DB 2; Length 378;
Best Local Similarity					100.0%; Pred. No. 2e-167;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MSDSYDDRMKDHMDERAPI	DAPPSLSDLKKAIPAHCFRRSAVSSCYVQDLITFLL	60	
Db	1	MSDSYDDRMKDHMDERAPI	DAPPSLSDLKKAIPAHCFRRSAVSSCYVQDLITFLL	60	
QY	61	YTVANTYIPLHPPPLVYLAWPVVFCQSCILGLWLGHCGHAFSEQWIDNAVGFVL	120		
Db	61	YTVANTYIPLHPPPLVYLAWPVVFCQSCILGLWLGHCGHAFSEQWIDNAVGFVL	120		
QY	121	HSALITPYFSWKYSHRKHANTNSLENEEVIYIPRTOSQLRTYSTYFELDNTPGRIILVI	180		
Db	121	HSALITPYFSWKYSHRKHANTNSLENEEVIYIPRTOSQLRTYSTYFELDNTPGRIILVI	180		
QY	181	MLTGLGFLYLLTNVSKKYDRFTNHPDPLSPITFERIQAVALSLGIYAVFGLKFLVQ	240		

Db 181 MLTGFPYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVIALSDLGIVAVFYGLKFLVQ 240

Qy 241 TKGFGWVCMYGPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLL 300

Db 241 TKGFGWVCMYGPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLL 300

Qy 301 NRVDHVTHTVHLHLPYIPHYHAKESAIKPILGDRMIDRTPPFKAMWREAKECIIY 360

Db 301 NRVDHVTHTVHLHLPYIPHYHAKESAIKPILGDRMIDRTPPFKAMWREAKECIIY 360

Qy 361 IEQDADSKHGTYWYHKM 378

Db 361 IEQDADSKHGTYWYHKM 378

RESULT 2

ID Q7XAL3\_HELAN PRELIMINARY; PRT; 377 AA.

AC Q7XAL3\_

DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 07-FEB-2006, entry version 14.

DE Delta12-fatty acid acetylase.

OS Helianthus annuus (Common sunflower).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;

OC Heliantheae; Helianthus.

OX NCBI\_TaxID=4232;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22674157; PubMed=12787248;

RX DOI=10.1046/j.1365-3113X.2003.01757.x;

RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;

RT "Fungal responsive fatty acid acetylases occur widely in

RT evolutionarily distant plant families.";

RL Plant J. 34:671-683(2003).

CC -----

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CC -----

DR EMBL; AY166773; AAC38032.1; -; mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.

DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.

DR GO; GO:0006636; P:fatty acid desaturation; IEA.

DR InterPro; IPR012261; FA\_acyl-CoA\_des.

DR InterPro; IPR005804; FA\_desat.

DR InterPro; IPR010257; FA\_desat\_sub.

DR Pfam; PF00487; FA\_desaturase; 1.

DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.

DR ProDom; PD001081; FA\_desat\_sub; 1.

KW Oxidoreductase.

SQ SEQUENCE 377 AA; 43751 MW; 832C8A129C6C2A55 CRC64;

Query Match 73.7%; Score 1537.5; DB 2; Length 377;

Best Local Similarity 72.8%; Pred. No. 46-121;

Matches 273; Conservative 41; Mismatches 54; Indels 7; Gaps 3;

Qy 8 RMKD----HMDERAPIDPAPFSLDLKKAIPAHCFERSAVWSSCYVVDLIITFLTYV 63

Db 6 RMSDSESGKNILIERVPIDP-PFTLSDLKKAIPAHCFERSVIRSSYVVHDLIVAVFPL 64

Qy 64 ANTYIPLPPPLVYLAWPYWYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVLHSA 123

Db 65 ANTYIPLPPTWAYLAWPYWYFQCASILTGLVWLGHECGHAFSDYQLIDDDIVGFVLHSA 124

Qy 124 LITPTFSWKYSHRKHANTNSLENEEVIYIPRTQSOLRTYSTVEFLDNTPGRLILIVIMLT 183

Db 125 LITPTFSWKYSHRKHANTNSLDNEEVIYIPKRAKAVVYS--KLNNPGRVFTLVFRLT 182

Qy 184 LGFPYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVIALSDLGIVAVFYGLKFLVQTKG 243

Db 183 LGFPYLLTNVSGKKYGRFANHFDPISPIFTRERIQVWISDIGILAVYLAKLLVEAKG 242

Qy 244 FGWVCMYGPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLLNRV 303

Db 243 AAWTCMYLIPVLGVHMFVLLITLHHTHLSPPHYDSTENWIRGALSTIDRDFGLNRV 302

Qy 304 PHDVHTHTVHLHLPYIPHYHAKESAIKPILGDRMIDRTPPFKAMWREAKECIIYEQ 363

Db 303 PHDVHTHTVHLHLSYIPHYHAKESAIKPILGVEFYKIDRTPIFKAMWREAKECIIYEP 362

Qy 364 DADSKHGTYWYHKM 378

Db 363 DEDSEHGTYWYHKM 377

RESULT 3

ID Q9SCG2\_CALOF PRELIMINARY; PRT; 377 AA.

AC Q9SCG2\_

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE (8,11)-linoleoyl desaturase (Fragment).

OS Name=des8.11;

OS Calendula officinalis (Pot marigold).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;

OC Calenduleae; Calendula.

OX NCBI\_TaxID=41496;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX TISSUE=developing seed;

RX MEDLINE=20086417; PubMed=10622705; DOI=10.1016/S0014-5793(99)01541-0;

RA Fritsche K., Hornung E., Peitzsch N., Renz A., Feussner I.;

RT "Isolation and characterization of a calendic acid producing (8,11)-

RT linoleoyl desaturase.";

RL FEBS Lett. 462:249-253(1999).

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CC -----

DR EMBL; AJ245938; CAB64256.1; -; mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.

DR GO; GO:0006636; P:fatty acid desaturation; IEA.

DR InterPro; IPR005804; FA\_desat.

DR InterPro; IPR010257; FA\_desat\_sub.

DR Pfam; PF00487; FA\_desaturase; 1.

DR ProDom; PD001081; FA\_desat\_sub; 1.

KW Oxidoreductase.

FT NON\_TER 377

SQ SEQUENCE 377 AA; 43615 MW; 1CBF7650955F26BF CRC64;

Query Match 73.0%; Score 1523.5; DB 2; Length 377;

Best Local Similarity 71.7%; Pred. No. 6.2e-120;

Matches 269; Conservative 45; Mismatches 54; Indels 7; Gaps 3;

Qy 8 RMKD----HMDERAPIDPAPFSLDLKKAIPAHCFERSAVWSSCYVVDLIITFLTYV 63

Db 6 RMSDSESGKNILIERVPIDP-PFTLSDLKKAIPAHCFERSVIRSSYVVHDLIVAVFYL 64

Qy 64 ANTYIPLPPPLVYLAWPYWYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVLHSA 123

Db 65 ANTYIPLIPTLAYLAWPYWYFQCASILTGLVWLGHECGHAFSDYQLIDDDIVGFVLHSA 124

Qy 124 LITPTFSWKYSHRKHANTNSLENEEVIYIPRTQSOLRTYSTVEFLDNTPGRLILIVIMLT 183

Db 125 LITPTFSWKYSHRKHANTNSLDNEEVIYIPKRAKVKIYS--KLNNPGRVFTLVFRLT 182

Qy 184 LGFPYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVIALSDLGIVAVFYGLKFLVQTKG 243

```
Db 183 LGFPLVLLNISKYKGRFANFDPMSPIFNDRERVQVLLSDFGLLAVFAIKLLVAAKG 242
QY 244 FGVMCMGVVPVIGNSFTIIVITYLHHTLSPHYDSTENWIKGALTITDRDFGLLNRV 303
Db 243 AAWINVMYAPVLGVSVFVLITYLHHTLSPHYDSTENWIKGALTITDRDFGLNRV 302
QY 304 FHDVTHVTHVHLFPYIPHYHAKASEAKIPILGDYRMDTRDPFFKAMWREAKECIIYEQ 363
Db 303 FHDVTHVTHVHLFISYIPHYHAKARDAIKPVLGEYKIDRTPIFKAMWREAKECIIYEP 362
QY 364 DADSKHKGTWYHKM 378
Db 363 DEDSEHKGVFWYHKM 377

RESULT 4
O65771_9ASTR PRELIMINARY; PRT; 374 AA.
AC O65771;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Delta 12 fatty acid epoxigenase.
OS Crepis palaestina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Crepis.
OX NCBI_TaxID=72611;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
RA Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gunnesson P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diiron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lemman M.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Y16283; CAA76156.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR012261; FA_acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desatase; 1.
DR PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_acyl-CoA_des; 1.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 374 AA; 43323 MW; 7764DB17BC7F426 CRC64;

Query Match 71.6%; Score 1493; DB 2; Length 374;
Best Local Similarity 70.1%; Pred. No. 2.3e-117;
Matches 260; Conservative 47; Mismatches 60; Indels 4; Gaps 2;

QY 8 RMDHMDRAIDPAPFSLKKAIPAHCFRRSAVWSSCYVQDLITFLTYVANTY 67
Db 8 RTSEKSMERVSVDPTFSLSELKQAIPEHCFQSRVIRSSYVQDLIAYIFYFLANTY 67
QY 68 IPHLPPLVLAWPVYVFCQSCILTLGLVLGHECGHAFSEYQWIDNAGFVLHSAALLTP 127
Db 68 IPTPLPTSLAYLAWPVYVFCQASVLTGLWILGHECGHAFSNYTFWDTVGFILHSAALLTP 127
QY 128 YFSWKYSHRKHANTNSLENEEYIPRTQSLRTYSTYEFDLNTPGRILILVIMLTGLFP 187
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Db 128 YFSWKFSHRNHSNTSSIDNDEVYIPKSKSLA--RIYKLLNPPGRLLVLIIMTLGPP 185
QY 188 LYLLTNVSGKYDRFTNHFDPPLSPFTFRERIQVALSDLGIVAVFYGLKFLVQTKGFGVW 247
Db 186 LYLLTNISGKYDRFANHFDPMSPIFKERERQVFLSDGLLAVFYGIKIVANKGAANV 245
QY 248 MCMYGVVPVIGNSFTIIVITYLHHTLSPHYDSTENWIKGALTITDRDFGLLNRVFDV 307
Db 246 ACMYGVPLGVFTFDDVITFLHHTHQSPPHYDSTENWIRGALSADRIDRDFGLNSVFHDV 305
QY 308 THTHVTHVHLFPYIPHYHAKASEAKIPILGDYRMDTRDPFFKAMWREAKECIIYEQDADS 367
Db 306 THTHVTHVHLFISYIPHYHAKARDAIKPILGDYRMDTRPILKAMWREGRECYIE--PDS 363
QY 368 KHKGTWYHKM 378
Db 364 KLKGVYVWYHKL 374

RESULT 5
FAD12_CREAL STANDARD; PRT; 375 AA.
AC O81331;
DT 01-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 2.
DT 07-FEB-2006, entry version 43.
DE Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepennate
DE synthase) (Delta-12 fatty acid acetylase).
OS Crepis alpina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Crepis.
OX NCBI_TaxID=72610;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
RA Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gunnesson P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diiron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
CC -!- FUNCTION: Changes the delta-12 double bond of linoleic acid into a
CC triple bond in the biosynthesis of crepennic acid.
CC -!- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepennate + A +
CC H(2)O.
CC -!- COFACTOR: Iron.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- TISSUE SPECIFICITY: Seed.
CC -!- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
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CC -----
DR EMBL; Y16285; CAA76158.2; -; mRNA.
DR InterPro; IPR012261; FA_acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
DR Fatty acid biosynthesis; Iron; Lipid synthesis; Membrane;
KW Oxidoreductase; Transmembrane.
FT CHAIN 1 375 Delta(12) fatty acid dehydrogenase.
FT TRANSMEM 54 74 /FTID=PRO_0000185424.
FT TRANSMEM 77 97 Potential.
```

FT	TRANSMEM	110	130	Potential.
FT	TRANSMEM	172	198	Potential.
FT	TRANSMEM	218	238	Potential.
FT	TRANSMEM	242	262	Potential.
FT	MOTIF	98	102	Histidine box-1.
FT	MOTIF	134	138	Histidine box-2.
FT	MOTIF	308	312	Histidine box-3.
SQ	SEQUENCE	375 AA;	43382 MW; B31F5A64DDC2926 CRC64;	
Query Match		68.3%;	Score 1424.5;	DB 1; Length 375;
Best Local Similarity		65.9%;	Pred. No. 1.4e-111;	
Matches 244;		Conservative 55;	Mismatches 68;	Indels 3; Gaps 2
Qy	8 RMDHDMDERAPIOPAPPSLDLKAIPACFRRAVSSCYVVQDLIITFLLYTVANTY	67	:	:
Dd	8 RTSQKPLMERVSUDP-PPTVSDGLKQAIPHCFKRSVIRSSYYIVHDIAIAYIFYELADKY	66	:	:
Qy	68 IPHLPPPIVLAWPYMFCQCILTLGVLVHGECGHAFSEYQWIDNAVGVFIHSALITP	127	:	:
Dd	67 IPIPLPAIYLAWPLYMFCQASIIITGLVAIGHCECHGAFFSDIQWVDVTVGFIHSFLMTFP	126	:	:
Qy	128 YFSWKYSRKHKHANTSLENEEVYTPRQSQRLTSTYTEFLDNTGRILLIIVIMLTGP	187	:	:
Dd	127 YFSWKYSHRNHANTSLEDNDEVYTPKSAAVALY--YKVLMHPGGRLIMEIFTTLP	184	:	:
Qy	188 LYLLTNISGKKYDRTHNFDPDSPFTPRERLOVALSDLGIVAVFGVKLFVQTGFPGW	247	:	:
Dd	185 LYLPTNISGKKYERFANHFDPMSPIFKSRERPQLLSDLGLLAIVYGVKLIAVAAGAAMV	244	:	:
Qy	248 MCMYGVPIVIGLNSFTVIITYLHTHSLSPHYDSTEWNMIKGALTITIDRDGFLINRVFDHV	307	:	:
Dd	245 TCIVGIPIVGVFIPDIITYLHTHLSLPHYDSSEWNLRGALSITIDRDGFLINSVLHDV	304	:	:
Qy	308 THTVHLHLFPYIPHYHAKEASEAIKPILDGYRMIDRTTFPKAMWREAKECIYIISQDADS	367	:	:
Dd	305 THTVMHMLFSYPHYHAKEARDAINTVLGDYDKIDRTPIPKAMWREAKECIFIBEKGR	364	:	:
Qy	368 KHGTGYTWTK	377	:	:
Dd	365 GSKGVYWNK	374	:	:

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RESULT 6
Q7XA09_9ASTR PRELIMINARY; PRT; 326 AA.
ID Q7XA09_9ASTR
AC Q7XA09
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Delta2-fatty acid acetylase (Fragment).
DI Dimorphotheca sinuata (African daisy).
OS Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae;
OC Calenduleae; Dimorphotheca.
OX NCBI_TaxID=112408;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22674157; PubMed=12787248;
RX DOI=10.1046/j.1365-3113X.2003.01757.x;
RA Caboon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
RL evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).
-----
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-----
CC EMBL; AY156777; AAC38036.1; --; Genomic_DNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
CC GO; GO:0006636; P:fatty acid desaturation; IEA.

```

[illegible]



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KW Oxidoreductase.
FT NON TER 326 1
SQ SEQUENCE 326 AA; 36030 MW; D355816CF4AA2829 CRC64;

Query Match 65.8%; Score 1369; DB 2; Length 326;
Best Local Similarity 73.8%; Pred. No. 5.7e-107;
Matches 242; Conservative 32; Mismatches 52; Indels 2; Gaps 1;

QY 31 KKAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPVLYLWVPVWFQCSQI 90
DB 1 KKAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPVLYLWVPVWFQCSQI 60

QY 91 LTGLWVIGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 150
DB 61 LTGLWVIGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 120

QY 151 YIPRTOSQURTSTYEFLLONTGORIILVIMLTGLGFPYLLTNVSGKKYDRFNNHDPPLS 210
DB 121 YIPKRSKVMYIS--KILNPPGRVFTLAFRLTLGFPYLLTNVSGKKYDRFNNHDPPLS 178

QY 211 PIPTERERIQVALSDIGIVAVFYGLKFLVOTKFGVMCMYGVPIVGLNSFIIVITLHHT 270
DB 179 PIPTERERIQVALSDIGIIVAVFYGLKFLVOTKFGVMCMYGVPIVGLNSFIIVITLHHT 238

QY 271 THLSPHYDSTENWIKGALTITDRDGFGLNRRVFDVTHVHLHLPYIPHYHAKESAE 330
DB 239 THLSPHYDSTENWIKGALTITDRDGFGLNRRVFDVTHVHLHLPYIPHYHAKESAE 298

QY 331 AIKPIGLDYRMIDRTPPFFKAMWREAKEC 358
DB 299 AINPVLGEYKIDRTPIFKAMWREAKEC 326

RESULT 8
Q7XA10 RUDHI PRELIMINARY; PRT; 326 AA.
AC Q7XA10;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE Delta12-fatty acid acetylase (Fragment).
OS Rubbeckia hirta (Black-eyed Susan).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Rudbeckia.
OX NCBI_TaxID=52299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22674157; PubMed=12787248;
RX DOI=10.1046/j.1365-3113.2003.01757.x;
RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
RT evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).
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CC -----
CC EMBL; AV166776; AAC38035.1; -; Genomic_DNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0016491; P:oxidoreductase activity; IEA.
CC GO; GO:0016717; P:oxidoreductase activity, acting on paired d. . .; IEA.
CC GO; GO:0006636; P:fatty acid desaturation; IEA.
CC InterPro; IPR005804; FA_desat.
CC InterPro; IPR010257; FA_desat_sub.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 326 1
SQ SEQUENCE 326 AA; 37865 MW; D3C65BAD9EF25783 CRC64;

Query Match 64.8%; Score 1351; DB 2; Length 326;
Best Local Similarity 72.3%; Pred. No. 1.9e-105;
Matches 237; Conservative 37; Mismatches 52; Indels 2; Gaps 1;

QY 32 KAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPVLYLWVPVWFQCSQI 91
DB 1 KAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPVLYLWVPVWFQCSQI 60

QY 92 TGLWVIGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 151
DB 61 TGLWVIGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 120

QY 152 IPTOSQURTSTYEFLLONTGORIILVIMLTGLGFPYLLTNVSGKKYDRFNNHDPPLS 211
DB 121 IPKRAKAAVYS--KILNPPGRVFTLAFRLTLGFPYLLTNVSGKKYDRFNNHDPPLS 178

QY 212 IETTERERIQVALSDIGIVAVFYGLKFLVOTKFGVMCMYGVPIVGLNSFIIVITLHHT 271
DB 179 IETTERERIQVALSDIGIIVAVFYGLKFLVOTKFGVMCMYGVPIVGLNSFIIVITLHHT 238

QY 272 HLSSPHYDSTENWIKGALTITDRDGFGLNRRVFDVTHVHLHLPYIPHYHAKESAE 331
DB 239 HLSSPHYDSTENWIKGALTITDRDGFGLNRRVFDVTHVHLHLPYIPHYHAKESAE 298

QY 332 IKPILGDYRMIDRTPPFFKAMWREAKEC 359
DB 299 IKPVLGEYKIDRTPIFKAMWREAKEC 326

RESULT 9
Q9SP28 VERGA PRELIMINARY; PRT; 383 AA.
AC Q9SP28;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN Name=FAD2-2;
OS Vernonia galamensis (Ironweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Vernoniaceae; Vernonia.
OX NCBI_TaxID=83960;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=10759541;
RA Hage T.G., Seither C., Hildebrand D.;
RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
RT encoding a microsomal oleate desaturase (FAD2) (accession nos.
RT AF188263 and AF188264) and functional expression in Saccharomyces
RT cerevisiae (PGR00-035).";
RL Plant Physiol. 122:1457-1457(2000).
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CC -----
CC EMBL; AF188264; AAF04094.1; -; mRNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0016717; P:oxidoreductase activity, acting on paired d. . .; IEA.
CC GO; GO:0050184; P:phosphatidylcholine desaturase activity; IEA.
CC GO; GO:0006633; P:fatty acid biosynthesis; IEA.
CC GO; GO:0006636; P:fatty acid desaturation; IEA.
CC InterPro; IPR012261; FA_acyl-CoA_des.
CC InterPro; IPR005804; FA_desat.
CC InterPro; IPR010257; FA_desat_sub.
CC Pfam; PF00487; FA_desaturase; 1.
CC PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
CC ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 383 AA; 44330 MW; 10D954DC084F7D41 CRC64;
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Query Match 61.9%; Score 1290.5; DB 2; Length 383;  
 Best Local Similarity 59.2%; Pred. No. 2.9e-100;  
 Matches 219; Conservative 68; Mismatches 80; Indels 3; Gaps 2;

QY 6 DDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVYVQDLITFLTYVAN 65  
 DB 13 DEKKAHEALQRPVQKPPFTVGDIKKAIPPHCFNRSVIRSFYVYDITISFIFYLAT 72  
 QY 66 TYIPLPPLVYLAWPVYVFCQSCILTLGLWLGECGHAFSEYQWIDNAGFVLHLSALL 125  
 DB 73 NYIPLPPLSVAVPVIWIFQGCVLTVGWVIAHECGHAFSDYQWLDVGLILHLSALL 132  
 QY 126 TPYFSWKYSHRKHANTNSLENEEYIIPRTQSLRTYSTYFELDNTGRILILVIMLTG 185  
 DB 133 VYFWSKYSHRRHHSNTGSIHDEVFVFKLSNVR--STARYLNNPPGRILTLVLTG 190  
 QY 186 FPLYLLTNVSKKGYDRFTNHFDPSPITERERRIOVALSDLGIVAVFVGLKFLVQTKGF 245  
 DB 191 WPLYLMFNVSGRYVDRFACHFDPNPSIYNSRERAIQIFISDAGILAVFVGLFKLAMAKGLT 250  
 QY 246 WYCMYGVVIGLNSFIIVITVYHHTLSSPHYDSTENWIKGALTTIDRDFGLLNRFVH 305  
 DB 251 WYLCMYGGLLVNGFVLITLQHTPSLPHYDTTEWDLRGALATIDRDYGLLNKVFH 310  
 QY 306 DVTHVHLHLPYIPHYHAKESAIAKPIILGDYRMDRTPPFKAMWREAKECIYIODEA 365  
 DB 311 NITDTHVAHLFSTMPHYHAMEATKVIKPIILGEYVQDGTSTIFKAMYRETKECIYVDKDE 370  
 QY 366 DSKHKGTYWY 375  
 DB 371 NVK-DGVYWY 379

RESULT 10  
 Q9SP29\_VERGA PRELIMINARY; PRT; 383 AA.  
 AC Q9SP29;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 24.  
 DE Delta-12 oleate desaturase (EC 1.3.1.35).  
 GN Name=FA2D-1;  
 OS Vernonia galamensis (Ironweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 OC Vernoniae; Vernonia.  
 OX NCBI\_TaxID=83960;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hage T.G., Seither C., Hildebrand D.;  
 RX PubMed=10759541;  
 RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.  
 RT encoding a microsomal oleate desaturase (FA2D) (accession nos.  
 RT AF188263 and AF188264) and functional expression in Saccharomyces  
 RT cerevisiae (PGR00-035).";  
 RL Plant Physiol. 122:1457-1457(2000).  
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 CC -----  
 CC EMBL; AF188263; AAF04093.1; -; mRNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
 DR GO; GO:0050184; F:phosphatidylcholine desaturase activity; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
 DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
 DR InterPro; IPR005804; FA\_desat.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.  
 DR ProDom; PD001081; FA\_desat\_sub; 1.

KW Oxidoreductase.  
 SQ SEQUENCE 383 AA; 44268 MW; C16B93BE7F94DA80 CRC64;

Query Match 61.6%; Score 1284.5; DB 2; Length 383;  
 Best Local Similarity 58.9%; Pred. No. 9.4e-100;  
 Matches 218; Conservative 68; Mismatches 81; Indels 3; Gaps 2;

QY 6 DDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVYVQDLITFLTYVAN 65  
 DB 13 DEKKAHEALQRPVQKPPFTVGDIKKAIPPHCFNRSVIRSFYVYDITISFIFYLAT 72  
 QY 66 TYIPLPPLVYLAWPVYVFCQSCILTLGLWLGECGHAFSEYQWIDNAGFVLHLSALL 125  
 DB 73 NYIPLPPLSVAVPVIWIFQGCVLTVGWVIAHECGHAFSDYQWLDVGLILHLSALL 132  
 QY 126 TPYFSWKYSHRKHANTNSLENEEYIIPRTQSLRTYSTYFELDNTGRILILVIMLTG 185  
 DB 133 VYFWSKYSHRRHHSNTGSIHDEVFVFKLSNVR--STARYLNNPPGRILTLVLTG 190  
 QY 186 FPLYLLTNVSKKGYDRFTNHFDPSPITERERRIOVALSDLGIVAVFVGLKFLVQTKGF 245  
 DB 191 WPLYLMFNVSGRYVDRFACHFDPNPSIYNSRERAIQIFISDAGILAVFVGLFKLAMAKGLT 250  
 QY 246 WYCMYGVVIGLNSFIIVITVYHHTLSSPHYDSTENWIKGALTTIDRDFGLLNRFVH 305  
 DB 251 WYLCMYGGLLVNGFVLITLQHTPSLPHYDTTEWDLRGALATIDRDYGLLNKVFH 310  
 QY 306 DVTHVHLHLPYIPHYHAKESAIAKPIILGDYRMDRTPPFKAMWREAKECIYIODEA 365  
 DB 311 NITDTHVAHLFSTMPHYHAMEATKVIKPIILGEYVQDGTSTIFKAMYRETKECIYVDKDE 370  
 QY 366 DSKHKGTYWY 375  
 DB 371 NVK-DGVYWY 379

RESULT 11  
 O82729 BOROF PRELIMINARY; PRT; 383 AA.  
 ID O82729;  
 AC O82729;  
 DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1998, sequence version 1.  
 DT 07-FEB-2006, entry version 26.  
 DE Delta-12 fatty acid desaturase.  
 OS Borage officinalis (Boraginaceae).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; lamiales; Boraginaceae; Borage.  
 OX NCBI\_TaxID=13363;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sayanova O., Shewry P.R., Napier J.A.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC EMBL; AF074324; AAC31698.1; -; mRNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
 DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
 DR InterPro; IPR005804; FA\_desat.  
 DR InterPro; IPR010257; FA\_desat\_sub.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.  
 DR ProDom; PD001081; FA\_desat\_sub; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 383 AA; 44048 MW; 13DF2BD876E7E5EF CRC64;

Query Match 61.3%; Score 1279; DB 2; Length 383;  
 Best Local Similarity 60.1%; Pred. No. 2.7e-99;



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QY 13 DMDERAPIDAPPSLDKKAIPAHCPRSAVSSCVVQDLIIITFLTYVANTYIPLP 72  
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QY 193 NVSGKKYDRFTNHFDPPLSPFTTERERIQVALSDLGIVAVFYGLKFLVQTKGFGVWVCMYGV 252  
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QY 253 VPVIGNSFLIIVTYLHHTLSSPHYDSTENWIKGALTTIDRDFGLLNRFVHDVTHV 312  
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QY 373 YWY 375  
Db 377 FWY 379

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AC Q6DMQ8;  
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
DT 11-OCT-2004, sequence version 2.  
DE Microsomal omega-6-desaturase.  
GN Name:FAD2;  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
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OX NCBI\_TaxID=4097;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wisconsin 38;  
RA Yang M., Zheng G., Zhang F., Xu Y.;  
RT "FAD2-silencing has pleiotropic effect on polar lipids of leaves and  
varied effect in different organs of transgenic tobacco.";  
RL Plant Sci. 170:170-177(2006).  
CC [2]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wisconsin 38;  
RA Yang M.F., Zhang F.Y., Zheng G.L., Xu Y.N.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
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EMBL: AY660024; AAT72296.2; -; mRNA.  
DR GO: GO:0016020; C.membrane; IEA.  
DR GO: GO:0016717; F.oxidoreductase activity, acting on paired d. . .; IEA.  
DR GO: GO:0006633; P.fatty acid biosynthesis; IEA.  
DR GO: GO:0006636; P.fatty acid desaturation; IEA.  
DR InterPro: IPR012261; FA\_acyl-CoA\_des.  
DR InterPro: IPR005804; FA\_desat.  
DR InterPro: IPR010257; FA\_desat\_sub.  
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DR FIRSF: FIRSF000347; FA\_acyl-CoA\_des; 1.  
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SQ SEQUENCE 383 AA; 43933 MW; 7D75199984305393 CRC64;  
Query Match 61.1%; Score 1274; DB 2; Length 383;  
Best Local Similarity 58.6%; Pred. No. 7.2e-99;  
Matches 211; Conservative 67; Mismatches 80; Indels 2; Gaps 1;  
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Db 22 EKVPYTKPFTVGDILKKAIPPHCFQSRSLVLSFSYVVDLVIAALFFYTASRYHLQP 81  
QY 76 VYLAWPVYWCQSCILTLGLWVLGHECHGHAFFSEYQWIDNAVGVLSALLTPYFSWKYSH 135  
Db 82 CYLAWPIYWCQCVCTGIVIAHECHGHAFFSDYQWLDLTVGLLHSAALVYFSWKYSH 141  
QY 136 RKHHANTNSLENEEVIPTQSQLRTYSTYEFDLNTPGRILILVIMLTGFPPLYLTNVS 195  
Db 142 RRHSNTGSLERDEVFVPKPSQLGWYSKY--LNNPGRVMSLTVTTLGWPLYLAFNVS 199  
QY 196 GKXDRFTNHFDPPLSPFTTERERIQVALSDLGIVAVFYGLKFLVQTKGFGVWVCMYGV 255  
Db 200 GRHYDRFACHFDKPSFYNDRLQIYISDAGIVAVMYGLYRLVAAKGVAVVVCYVG 259  
QY 256 IGLNSFLIIVTYLHHTLSSPHYDSTENWIKGALTTIDRDFGLLNRFVHDVTHV 315  
Db 260 LINGVFLVLTLYLQHTQPSLPHYDSEWDLKGLALATVDRDYGLNKLHNTDTHV 319  
QY 316 LFPYIHYHAKSEAIKPIGLDYRMDTRPFFKAMWREAKECIYIEQDADSKHKT 375  
Db 320 LFTMPHYHAEATKAIPILGDYQCDRTVPFKAMWREAKECIYVEADSGDNKGV 379

RESULT 13  
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AC Q2VG85;  
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.  
DT 10-JAN-2006, sequence version 1.  
DT 07-MAR-2006, entry version 4.  
DE Delta12-fatty acid desaturase.  
OS Jatropha curcas.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Malpighiales; Euphorbiales; Crotonoideae;  
OC Jatrophaeae; Jatropha.  
OX NCBI\_TaxID=180498;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Qing R., Luo L., Luo T., Xu Y., Tang L., Li H., Chen F.;  
RT "Identification and characterization of a novel delta12-fatty acid  
desaturase gene from higher plant Jatropha curcas.";  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
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EMBL: DQ157776; ABA41034.1; -; mRNA.  
KW Oxidoreductase.  
SQ SEQUENCE 383 AA; 44473 MW; 8ACD0F2444017D92 CRC64;  
Query Match 61.1%; Score 1274; DB 2; Length 383;  
Best Local Similarity 59.2%; Pred. No. 7.2e-99;  
Matches 213; Conservative 63; Mismatches 82; Indels 2; Gaps 1;  
QY 16 ERAPIDPAPPSLDKKAIPAHCPRSAVSSCVVQDLIIITFLTYVANTYIPLP 75  
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QY 76 VYLAWPVYWCQSCILTLGLWVLGHECHGHAFFSEYQWIDNAVGVLSALLTPYFSWKYSH 135  
Db 82 SYVAMPYWSLQCVLTGIVIAHECHGHAFFSDYQWLDLTVGLLHSAALVYFSWKYSH 141  
QY 136 RKHHANTNSLENEEVIPTQSQLRTYSTYEFDLNTPGRILILVIMLTGFPPLYLTNVS 195



Db 244 LGWVLA MYGGLVAVNGFLVLTITFLOTHASLPHYDSTENDWLRGALATIDRDYGLNKV 303  
Qy 304 FHDVTHVHLHLPYI PHYHAKASEATKPIILGDYRMIDRTPTPFKAMWREAKECIYIEQ 363  
Db 304 FHNITDTHVHLHLPYI PHYHAKASEATKPIILGDYRMIDRTPTPFKAMWREAKECIYIEQ 363  
Qy 364 DADSKHKGTWY 375  
Db 364 DAEVK-DGVWY 374

Search completed: September 22, 2006, 19:43:23  
Job time : 304 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2006, 23:03:22 ; Search time 7201 Seconds  
(without alignments)  
10918.286 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
Sequence: 1 gtaggtttgggtcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_hic:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gse1:\*
- 12: gb\_gse2:\*
- 13: gb\_gse3:\*
- 14: gb\_gse4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564.6	40.2	1047	10	DW097268 CLPX7268
2	509.8	36.3	982	10	DW097410 CLPX8434
3	503.2	35.8	941	10	DW158633 CLV10747
4	495.4	35.2	937	10	DW085008 CLPX8050
5	493.2	35.1	921	10	DW093963 CLPX5158
6	493.2	35.1	922	10	DW094502 CLPX5660
7	493.2	35.1	927	10	DW097606 CLPX8633
8	492.2	35.0	922	10	DW094732 CLPX5873
9	491.8	35.0	906	10	DW093673 CLPX4893
10	491.6	35.0	928	10	DW089055 CLPX1380
11	485.2	34.5	898	10	DW090169 CLPX14207
12	483.4	34.4	893	10	DW089237 CLPX13349
13	483	34.4	942	10	DW097931 CLPX8961
14	481.2	34.2	919	10	DW089183 CLPX13299
15	480.8	34.2	908	10	DW096275 CLPX7316
16	479.4	34.1	885	10	DW128132 CLSX4996
17	479	34.1	906	10	DW090949 CLPX2215
18	475.8	33.8	906	10	DW097416 CLPX8440
19	475.4	33.8	953	10	DW097829 CLPX8857

20	474.4	33.7	878	10	DW084498
21	471.8	33.6	906	10	DW098114
22	470.4	33.5	863	10	DW114098
23	469.4	33.4	907	10	DW093425
24	465	33.1	866	10	DW084816
25	464.8	33.1	902	10	DW094062
26	464.2	33.0	964	10	DW119170
27	464	33.0	866	10	DW084758
28	464	33.0	871	10	DW079511
29	461	32.8	886	10	DW092156
30	459.8	32.7	897	10	DW094175
31	455	32.4	897	10	DW091892
32	454.6	32.3	879	10	DW097724
33	448	31.9	906	10	DW097104
34	446	31.7	849	10	DW094401
35	443.2	31.5	691	3	BQ994479
36	440	31.3	799	10	DW096751
37	437.2	31.1	685	10	DT211274
38	436.2	31.0	862	10	DW094388
39	434.8	30.9	849	10	DW098230
40	433	30.8	823	10	DW093011
41	428.6	30.5	797	10	DW087447
42	423.4	30.1	798	10	DW048664
43	417	29.7	859	10	DW058651
44	416.4	29.6	844	10	DW092317
45	415.6	29.6	785	10	DW097877

ALIGNMENTS

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LOCUS CLPX7268.b1 C10.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA  
DEFINITION Clone CLPX8290, mRNA sequence.  
ACCESSION DW097268  
VERSION DW097268.1 GI:83895188  
KEYWORDS EST.  
SOURCE Lactuca perennis  
ORGANISM Lactuca perennis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
REFERENCE 1 (bases 1 to 1047)  
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
Ellison,P., Kolkman,J., Slabaugh,W.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://comgenomics.ucdavis.edu/  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
FEATURES  
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/lab\_host="E.coli"  
/clone\_lib="CLP(XYZ) lettuce perennis"  
/note="Vector: pBRCDNASFIAB; The standard library was  
constructed from multiple sources of RNA from a single









SOURCE	Lactuca perennis	Db	448	CCCTATTTCTTTGGAAATACAGCCATCGAATACCATGCCAACACAAATTCACCTTGAT	507
ORGANISM	Lactuca perennis	Qy	530	AACGAGGAGTTTACATCTCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACGAA	589
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.	Db	508	RACGATGAGTTTACATCTCTAAACGCAAGTCCAAAGTCACGCTTACTCAA-----AA	561
AUTHORS	1 (bases 1 to 921) Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevallier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.	Qy	590	TTTCTTGACAAACGCGCTGGTCCGATCCCTCATCTCTGGTGCATCATGTTAACCTTAGATTT	649
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/	Db	562	CTTCTTAAACACCCACCTGGTGGAGTGTTCACCTTTGGTGTGGTGGTGGTGGTGGTGG	621
JOURNAL	Unpublished (2002)	Qy	650	CTTTTATACCTCTTACGAAATCTTTCAGGCAAGAGTACGATAGATTTTACCACCACTTT	709
COMMENT	Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Amondson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akosik@ucdavis.org [michelmore@vegmail.ucdavis.edu] Library was sequenced at Joint Genome Institute, Walnut Creek CA, using ABI 3730 machines.	Db	622	CTTTTATACCTCTTAACTAATATTTCTGCAAAAATACGGAAGATTTGCCAACCACTTT	681
FEATURES	Location/Qualifiers	Qy	710	GATCCATTGAGCCCGATCTTCCAGCGGTGAGCGAATCCAGGTTGCGTTATCAGATCTT	769
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		Db	742	GGTCTTCTTGGCGTCTTTTATGCAATTAACCTTGCTGTAGAAAAGAAAGAGATTGCTTGG	801
		Qy	830	GTGATGTGCATGTATGGAGTTCAGTGATAGTCTGAATTCCTTATTATCGTAATCACT	889
		Db	802	GTGACCTGCATATATGGAGTACAGTGTAGGCGTATTTATCTTTTGGTTGATCAGC	861
		Qy	890	TATCTGCACCACACATCTGTCTGTCACCCCATTCAGATTCAACCGAATGGAACTGGATC	949
		Db	862	TATTTGCACCACACTCATCTCAGTCATTCCTCTACTATGATTCAACCGAATGGAACTGGATC	921
		RESULT 6	DM094502	922 bp mRNA linear EST 22-DEC-2005	
		LOCUS	CLPY5660	bi G24.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA	
		DEFINITION	DM094502	clone CLPY5660, mRNA sequence.	
		ACCESSION	DM094502.1	GI:83892422	
		VERSION	DM094502.1		
		KEYWORDS	EST.		
		SOURCE	Lactuca perennis		
		ORGANISM	Lactuca perennis		
		REFERENCE	1 (bases 1 to 922) Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevallier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.		
		AUTHORS	Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Amondson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akosik@ucdavis.org [michelmore@vegmail.ucdavis.edu] Library was sequenced at Joint Genome Institute, Walnut Creek CA, using ABI 3730 machines.		
		TITLE			
		JOURNAL			
		COMMENT			
		FEATURES	Location/Qualifiers		
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genotype. cDNAs were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>

## ORIGIN

Query Match 35.1%; Score 493.2; DB 10; Length 922;  
Best Local Similarity 76.0%; Pred. No. 1.8e-114;  
Matches 638; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

QY 110 GATCGAATGAAGATCATGATATGACGACGAGCCCGATGATCGCGGCCATCTCG 169  
DB 92 GATCCATCTAAGGACACGATATATAAAGCGTGCCGGTGA---GCCACCATCTCA 148  
QY 170 TTAAGTGATCTAAGAAAGCAATCCCTGCACATTGCTTCCGGCGATCCGCGTCTGGTCA 229  
DB 149 CTAAGTGATCTCAAGAAAGCAATCCCTGCCATGCTTGGAGCGTCACTATCGTTCA 208  
QY 230 TCCTGCTAGTGTGAGTTCAGGATCTCATATATCACTTCTCTTTTATACACGGTCCCAACACC 289  
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QY 290 TACATCTCTACCTCCCTCTCTAGTTTACTTACTAGTACGCGGTTTACTGTTTTCG 349  
DB 269 TATATTCCTTATCTTCTTATCTCTAGCTTACTTACTAGTACGCGGTTTACTGTTTTCG 328  
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QY 410 AGTGAGTACCAAGTGTGATTAACCCGTTGGATTCGTCTCTCAATTCGGCTCTCTCACC 469  
DB 389 AGTGACTACCAATGATGATGATACAGTTCGGCTTTCATCTTCTCTCTCTCTCACC 448  
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RESULT 7  
DW097606  
LOCUS

DW097606 927 bp mRNA linear EST 22-DEC-2005

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CLPY8633.b1.B23.ab1.CLP(XYZ) lettuce perennis Lactuca perennis cDNA  
Clone CLPY8633, mRNA sequence.  
DW097606.  
DW097606.1 GI:83895526  
EST.  
Lactuca perennis

## REFERENCE

1 (bases 1 to 927)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
Unpublished (2002)

## AUTHORS

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Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.

## JOURNAL

Location/Qualifiers  
1. 927  
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/mol\_type="mRNA"  
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/clone\_lib="CLP(XYZ) lettuce perennis"  
/note="Vector: pBRCNAsf1AB; The standard library was  
constructed from multiple sources of RNA from a single  
genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>"

## FEATURES

## source

Query Match 35.1%; Score 493.2; DB 10; Length 927;  
Best Local Similarity 76.0%; Pred. No. 1.8e-114;  
Matches 638; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

QY 110 GATCGAATGAAGATCATGATATGACGACGAGCCCGATGATCGCGGCCATCTCG 169  
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DB 154 CTAAGTGATCTCAAGAAAGCAATCCCTGCCATTTCTTTCGAGCGCTCACTATCGTTCA 213  
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Query Match 35.1%; Score 493.2; DB 10; Length 927;  
Best Local Similarity 76.0%; Pred. No. 1.8e-114;  
Matches 638; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

QY 110 GATCGAATGAAGATCATGATATGACGACGAGCCCGATGATCGCGGCCATCTCG 169  
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## RESULT 8

DW094732  
LOCUS  
DEFINITION  
CLP55873.b1 B05.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA  
clone CLP55873, mRNA sequence.

ACCESSION  
DW094732.1 GI:83892652

VERSION  
EST.

KEYWORDS  
Lactuca perennis

SOURCE  
Lactuca perennis

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.

1 (bases 1 to 922)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkmann, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished (2002)

## JOURNAL

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Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

Library was sequenced at Joint Genome Institute, Walnut Creek CA,

using ABI 3730 machines.

## FEATURES

source

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/organism="Lactuca perennis"

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constructed from multiple sources of RNA from a single  
genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgpsdb.ucdavis.edu/>

## ORIGIN

Query Match 35.0%; Score 492.2; DB 10; Length 922;  
Best Local Similarity 75.8%; Pred. No. 3.3e-114;  
Matches 637; Conservative 0; Mismatches 194; Indels 9; Gaps 2;  
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constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"

ORIGIN
Query Match 35.0%; Score 491.6; DB 10; Length 928;
Best Local Similarity 75.7%; Pred. No. 4.7e-114;
Matches 637; Conservative 0; Mismatches 195; Indels 9; Gaps 2;

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RESULT 12
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  cDNA clone CLP13349, mRNA sequence.
DW089237
ACCESSION
  DW089237.1 GI:83887157
VERSION
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  1 (bases 1 to 893)
  Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
  Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
  Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
  Lai,Z., Church,S., Jackson,L. and Bradford,K.
  Lettuce and Sunflower ESTs from the Compositae Genome Project
  http://compgenome.ucdavis.edu/
  Unpublished (2002)
  CONTACT: Alexander Kozik [R.W.Michelmore]
```

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University of California at Davis (UCD)  
Amundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.

Location/Qualifiers  
source  
1. .893  
/organism="Lactuca perennnis"  
/mol\_type="mRNA"  
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cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>

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Query Match 34.4%; Score 483.4; DB 10; Length 893;  
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Lai, Z., Church, S., Jackson, L., and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
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transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>"

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Query Match 34.2%; Score 481.2; DB 10; Length 919;  
Best Local Similarity 75.8%; Pred. No. 2.1e-111;  
Matches 637; Conservative 0; Mismatches 193; Indels 10; Gaps 3;

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1 (bases 1 to 908)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
Location/Qualifiers  
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constructed from multiple sources of RNA from a single  
genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>"

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ORIGIN

Query Match 34.2%; Score 480.8; DB 10; Length 908;

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2006, 00:03:35 ; Search time 300 Seconds  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	464.2	33.0	1647	8	US-11-216-545-4819
3	462.6	32.9	1517	9	US-11-056-355B-52711
4	462.6	32.9	1669	8	US-11-216-545-4818
5	462.2	30.3	1451	9	US-11-056-355B-39927
6	426.2	30.3	1459	9	US-11-056-355B-98545
7	426.2	30.3	1459	9	US-11-056-355B-109784
8	426.2	30.3	1617	6	US-10-547-086-17
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17	390.2	27.8	1470	8	US-11-216-545-2763
18	390.2	27.8	4497	7	US-11-369-993-15
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40	180.8	12.9	544	8	US-11-058-746-2	Sequence 2, Appli
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## ALIGNMENTS

## RESULT 1

US-11-369-993-3  
; Sequence 3, Application US/11369993  
; Publication NO. US20060191042A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillattl, Joanne, J.  
; TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of P  
; TITLE OF INVENTION: with Modified Polynsaturated Fatty Acids  
; FILE REFERENCE: 16518.056  
; CURRENT APPLICATION NUMBER: US/11/369,993  
; CURRENT FILING DATE: 2006-03-08  
; PRIOR APPLICATION NUMBER: US/10/176,149  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/151,224  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: US 60/172,128  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: US 09/638,508  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
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; ORGANISM: Glycine max  
US-11-369-993-3

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US-11-216-545-4819

Sequence 4819, Application US/11216545

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; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaire, Paul L
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Soybeans
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: US 60/606,062
; PRIOR FILING DATE: 2004-08-31
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Best Local Similarity 62.3%; Pred. No. 5.8e-90;
Matches 749; Conservative 0; Mismatches 448; Indels 6; Gaps 1;
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Db 611 GTATCATGTGGTACTCTAAATAC-----CTTAACAATTCACCAAGGAGAGTCTCTCATCT 664
QY 624 TGGTCATCATGTTAACTTTAGGATTTCTTTTATACCTTTAACGAATGTTTTCAGGCAAGA 683
Db 665 TTGGGTCACCTCAGCTTGGTGGCCCTTGTACTTTGGCTTTTAAATGTTTCTGGAAGGC 724
QY 684 AGTACGATGATTTACCAACCACTTTGATTCATTTGAGCCCGATCTTTCACCGAGGTGAGC 743
Db 725 CTTATGATAGATTTGCTTGGCCATGATGACCCCTTATGGTCCCATTTACTCTGACCGAGAAC 784
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Qy	744	GAATCAGGTTGGCTTATCAGATCTTGGTATCGTTGCGAGTGTGTTTACCGGACTCAAGTTTC	803
Db	785	GACTTCAAAATATATATATACAGATGCAAGGAGTACTTTCAGTATGCTATGGGCTTTTTCGTGTC	844
Qy	804	TTGTACAAACAAAGAGTATTTGGTTGGGTGATGTGCATGTATGCAGTTTCCAGTGATAGGTC	863
Db	845	TTGCCATGGCAAAAGGGCTTGCCTGGGTGGTGTGTGTTTATGGAGTTCCATTGCTTGTGG	904
Qy	864	TGAATTCCTTCATTATTCGTTAATCACTTATCTGCACCAACACACATCTGTCTGTCACCCCAAT	923
Db	905	TCAATGGATTTTGGTGTTCATTACATTTTTCGAGCACACTCACCCCTGCATTGGCCACACT	964
Qy	924	ACGATTCACCGAATGGAATCGGATCAAAGGAGCCTTGACCACAATCGACAGAGATTTTCG	983
Db	965	ACACTTCTCTGAGTGGGACTGGTTGAGAGGGAGCTTTAGCAACAGTGGATAGAGATTATG	1024
Qy	984	GTCTCCTGAATCGGTTTTTCCACGAGCTTACACACCCACGCTGTGTGCACCATTTGTTTC	1043
Db	1025	GAATCTGGAACAGGTTCTTCATATATATTAAGACACTCATGTAGTCTCATCTTGTCT	1084
Qy	1044	CCTACATTCACCATTTATCATGCAAGGAGGCAAGCGAGGCCATCAAGCCCAATCTTGGGTG	1103
Db	1085	CCACATGTCACATTTATCATGCAATGAGGCGGCAAAAGGCAATAAAGSCCATCTTGGGAG	1144
Qy	1104	ATTACAGGATGATCGACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGGCCCAAGAAAT	1163
Db	1145	AGTATTATCGTTTGTATGGGACTCCATTTGTCAAGGCAATGTGTGAGAGAGGCAAGAGAGT	1204
Qy	1164	GCATTTACATCGACAGATGCGACAGCAAGCAAGCAAGGACATATTTGGTACCATAAAA	1223
Db	1205	GTATTTATGTGGAGCCAGATCAAAGTACTCAGAGCAAAAGGTGATTTTGTGTACAACAATA	1264
Qy	1224	TGT 1226	
Db	1265	AGT 1267	
RESULT 3			
US-11-056-355B-52711			
; Sequence 52711, Application US/11056355B			
; Publication No. US20060150283A1			
; GENERAL INFORMATION:			
; APPLICANT: Brover, Vyacheslav			
; APPLICANT: Alexandrov, Nikolai			
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding			
; TITLE OF INVENTION: Polypeptides Encoded Thereby			
; FILE REFERENCE: 2750-1590PUS2			
; CURRENT APPLICATION NUMBER: US/11/056,355B			
; CURRENT FILING DATE: 2005-02-14			
; PRIOR APPLICATION NUMBER: 60/544,190			
; PRIOR FILING DATE: 2004-02-13			
; NUMBER OF SEQ ID NOS: 119966			
; SEQ ID NO 52711			
; LENGTH: 1517			
; TYPE: DNA			
; ORGANISM: Glycine max			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)..(1517)			
; OTHER INFORMATION: Ceres Seq. ID no. 15177298			
US-11-056-355B-52711			
Query Match 32.9%; Score 462.6; DB 9; Length 1517;			
Best Local Similarity 62.2%; Pred. No. 1.3e-89;			
Matches 748; Conservative 0; Mismatches 449; Indels 6; Gaps 1;			
Qy	24	TCAGTGTTCGACCGAAATCCAAACCATTTTCTAATTTTGGATTTTCAGAAATCTGGGAGAAG	83
Db	40	TCTGTGGCTCTAACAAACATTTCTCGTTTCACACTTCAGATTGTGTGATGGGGCGG	99
Qy	84	GTAGCAGAATGTCGGATTTCATATGATGATGAAAGATCATGATATGGAACGACGAG	143
Db	100	GTGGCCGAACTGATGTTTCTCTCCCAACAGAAAGTCAGAGTTTGACCTTTTGAAGCGGG	159

Qy	144	CCCCGATTGATCCGGCGGCATTCTCTGTTAAGTGATCTAAAGAAAGCAATCCCTGCGACATT	203
Db	160	TGCCATTTTGAAAACCTCCATTAGTCTCAGCCAAATCAAGAAAGGTCATTCCACCTCACT	219
Qy	204	GCTTCGGCGGATCCGGCTGTGTGTCATCTGTCTACGTAGTTTACAGGATCTCATTTACACCT	263
Db	220	GTITCCAGCGTTCTGTTTCCGGCTCATTTCTCTATGTTGTTTACGACCTCACCATAGCCT	279
Qy	264	TCCTTTTATACAGGTGCGCAACACCATACATTCTCCACCTCCTCTCTCTCTAGTTTACT	323
Db	280	TCTGCTCTATTATGTTGCCACCAATTAATTCACCTCCCTCCAGCCCTCTCTCTTCT	339
Qy	324	TAGCATGGCGGTTTACTGTGTTTGGCAATCTTTGGCATCTCTCACTGGTTTATGGGTCTCTG	383
Db	340	TGGCATGGCCAAATCTACTGGGCTGTCCAAAGTTGTCATCTTACTTGGAGTTTGGGTCAATG	399
Qy	384	GCCATGAATGGCGCCATCATGCTTTAGTTCAGTACCAGTGGATTGATAACGCCGTTCGAT	443
Db	400	CCCATGAGTGGGCCACCATGTCATTCAGTGACTACCAGTTGCTTGATGATTTGTTGGCC	455
Qy	444	TCGTCTCTCAATTCGGCTCTCTCACCCCTTACTTTTCTTGGAAATAACAGCCATCGAAAGC	503
Db	460	TTGTCTCTCACTCCGGTCTCTAGTCCCATCTTTTCATGGAATAACAGCCATCGCCGTC	519
Qy	504	ACCATCAAAACAAATTCATCTCGAAACGAGGAAGTTTACATTCCTAGAACTCAGTCCC	563
Db	520	ACCACTCCAACACTGGTTCTCTTGAGCGGATGAAGTATTTGTGCCAAAGCAGAAGTCCCT	579
Qy	564	AGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACAGCCCTGGTCGAAATCCTCATCT	623
Db	580	GTATCAAGTGGTACTCTAAATAC-----CTTTACAAATCTCCAGGCAGAGTCTCTCACTC	633
Qy	624	TGCTCATCATGTTAACTTTAGGATTTCTTTATACCTCTTTAACGAATGTTTCAGGCAAGA	683
Db	634	TTGCTGTCACTCCCTCACACTTGGTTGGCCCTTGACTTGGCTTTAAATGTTTCTGGAAGGC	693
Qy	684	AGTACGATAGATTACCAACACTTTTGATCCATTGAGCCCGCATCTTCACCGAGCGTAGC	743
Db	694	CTTATGATAGATTGCTTTGCCACTATGACCCATATGGTCCCAATTAATCTCTGATCGTGAAC	753
Qy	744	GAATCCAGGTTCGGTTATCAGATCTTGGTATTCGTTGCGAGTGGTTTACGGAATCAAGTTTC	803
Db	754	GACTTCAAAATATATATACAGATGCGAGGAGTACTTGCAGTATGCTATGGGCTTTTCCGTC	813
Qy	804	TTGTACAAACAAAGGATTTGGTTGGTGATGTCATGTATGAGTTTCCAGTGTATAGTCTC	863
Db	814	TTGCCATGGCAAAAGGACTTGGCTGGGTGGTGTGTGTTTATGAGTTTCCATTCGTAGTGG	873
Qy	864	TGAATTCCTTCATTATCGTAATCACTTATCTGCACCAACACACATCTGCTCGTCAACCCCAT	923
Db	874	TCAATGGATTTTGGTTGATTTACATCTTTGACGCAATCTCACCTTCGATTCGCACATT	933
Qy	924	ACGATTCAAACCGAATGGAATCGGATCAAGAGGACCTTGACCACAAATCGACAGAGATTCG	983
Db	934	ACACTTCTCTGATGGGACTGGTTGAGAGGAGCTTTTAGCAAACAGTGGATAGAGATTATG	993
Qy	984	GTCTCTGAAATCGGGTTTTCCAGCATGTTACACACCCACAGTGTGTCACCATTTGTTTC	1043
Db	994	GAATTCCTGAAACAAGGCTTCCATAAATTTACAGACACTCAATGATGACATCATCTGTGTTCT	1053
Qy	1044	CCTACATTCACATTAATCATGAAAGAGGACGAGCGGCATCAAGCCAAATCTTTGGGTG	1103
Db	1054	CCAAATGCCCACATTAATCATGCAATGAGGCTTCAAAAGGCATAAAMCCCATTTTGGGAG	1113
Qy	1104	ATTAACAGATGATCGACAGGACTCCATTTTTCAAAGCAATGTGTGGAGAGCGCCAAAGGAAT	1163
Db	1114	AGTATTATCCGTTTGATGAGACTCCATTTGTCAAGCAATGTGTGAGAGAGCGAAGAGAT	1173
Qy	1164	GCATTTACATCGAGCAAGATGCGACAGCAAGCAAGGAGCAATATTTGGTACCATAAAA	1223
Db	1174	GTATTTATGTGGAGCCAGATCAAAAGTACCGAGAGCAAGGTGTATTTTGTGTACCAACATA	1233

	Query Match	32.9%	Score 462.6	DB 9	Length 1517
	Best Local Similarity	62.2%	Pred. No. 1.3e-89		
	Matches 748	Conservative	0	Mismatches 449	Indels 6
					Gaps 1
Qy	24	TCAGTGTTCGACCGAATCCAA	CCGATTTCTAAATTTGGATTCAGAAATCTGGGAGAAG	83	
Db	40	TCTGTGCGCTCTAACAAACATTC	TCGTTACACTTCAGATTTGTGAAGATGGGGCGG	99	
Qy	84	GTAGCAGATGTTCGGATTCAT	TGATCGATCGAATGAAAGATCATCATATGGACGAAACGAG	143	
Db	100	GTGGCCGAACTGATGTTCTCT	CTCCCAACAGGAAGTCAGAGTTTGACCCTTTGAAGCGGG	159	





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/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1451)
/ OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
/ OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-39927

Query Match      30.3%; Score 426.2; DB 9; Length 1451;
Best Local Similarity 61.0%; Pred. No. 7.5e-82;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

QY 65 TTCAGAAATCTGGAGAGGTAGCAGAAATGTCGGATTTCATATGATCGAATGAAGAT 124
DB 144 TCAGAAATCATGGGTGAGGTGAGAAATGCGGGTTCCTTCTTCCAGAAATCGGAA 203
QY 125 CATGATATGGACGAAACGAGCCCGATTGATGCCGCGCAATTCGCTTAAAGTGAATCAAAG 184
DB 204 ACCGACACCAAAAGCGTGGCGTGGAGAAACCGCCTTCTCGGTGGGAGATCTGAAG 263
QY 185 AAGCAATCCCTGCAATTCGTCCTGGCGGATCGCGCTCTGCTGTCATCTGCTACGTAGTT 244
DB 264 AAGCAATCCCGCGCATTTGTTCAAACGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 323
QY 245 CAGGATCTCATTTATCACTCTCTTTTATACAGGTGCGCAACACCTACATTTCTCTACCTC 304
DB 324 AGTGACATCATTTATAGCCTATGCTTCTACTAGTCGCCACCAATTAATTTCTCTCTCTC 383
QY 305 CTTCTCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTTCGCAATCTTGCACTCTC 364
DB 384 CTTGAGCTCTCTTACTTCTGCTTGGCCACTCTATTTGGCCCTGTCAAGCTGTGTCTTA 443
QY 365 ACTGGTTTATGGTCTCTCGGCCATGAATGGGCCATCATGCCCTTTAGTGAGTACCAAGTG 424
DB 444 ACTGGTATCTGGTCTATAGCCCAAGATGCGGTCCACGACATTCAGCGACTACCAATGG 503
QY 425 ATTGATAACGCGTGGATTCGCTCCATTCGCTCTCTCTACCCCTTACTTTCTCTGG 484
DB 504 CTGGATGACACAGTTGGTCTTATCTTCCATTCCTCTCTCTCTCTCTCTCTCTCTCTGG 563
QY 485 AAATACAGCATCGAAAGACCATGCAAAACAAATTCATCTGAAACGAGGAAGTTTAC 544
DB 564 AGATATAGTATCGCGCTACCATTCACACCTGGATTCCTCGAAAGATGAAGTATTT 623
QY 545 ATTCTTAGAATCCAGTCCAGCTCAGGACTTACTCCACATACAGAAATTTCTTGACACAG 604
DB 624 GTCCCAAGCAGAAATCAGCAATCAAGTGTAGCGGAATAC-----CTCAACACCCCT 677
QY 605 CTGCTGTAATCTCTATCTTGGTGCATCATGTTAACTTAGATTTCTTTTATACCTTTA 664
DB 678 CTTGGACGCATCATGATGTTAAACCGTCCAGTTTGTCTCGGGTGGCCCTTGACTTAGCC 737
QY 665 ACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTGATCCATTTAGCCCG 724
DB 738 TTTAAGCTCTCTGGCAGACGGTATGAGGGTTCGCTTGCCATTTCTTCCCAAGCTCC 797
QY 725 ATCTTCACCGAGCGTGAGCGAAATCCAGGTTTCGCTTATCAGATCTTGATTCGTTGCAAGT 784
DB 798 ATCTCAATGACCGCAGAACCGCTCCAGATATACCTCTCTGATCGGCTATTTAGCCGTC 857
QY 785 TTTTACGAGTCAAGTTTCTTGTAACAAAGAGATTTGGTTGGGTGATGTGCATGTAT 844
DB 858 TGTTTTGGTCTTTACCGTTTACGCTGTCACAAAGGATGCGCTCGATGATCTGCTCTAC 917
QY 845 GGAGTTCCAGTATAGTCTGAATTCCTTCAATTAATGATATCTGTAATCACTTATCTGACACACA 904
DB 918 GGAGTACCGCTTCTGATAGTGAATGGTTCTCTGCTTTGATCACTTACTTTGACGACACT 977
QY 905 CATCTCTGCTCAGCCCAATACGATTCAAACCGAATGGAATCGAATCAAAGGAGCTTTGACC 964
DB 978 CATCCCTCTGCTCTCACTACGATTTATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCT 1037
QY 965 ACAATCGACAGAGATTTTCGCTCTCTGAAATCGGGTTTTTCAACGATTAACACACCCAC 1024
DB 1038 ACGTAGACAGAGACTACGGAATCTTTGAACAAAGGTGTTTCCAAACATTTACAGACACAC 1097

RESULT 6
US-11-056-355B-98545
; Sequence 98545, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98545
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1459)
; OTHER INFORMATION: Ceres Seq. ID no. 13600976
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1459)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
; OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-98545

Query Match      30.3%; Score 426.2; DB 9; Length 1459;
Best Local Similarity 61.0%; Pred. No. 7.5e-82;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

QY 65 TTCAGAAATCTGGAGAGGTAGCAGAAATGTCGGATTTCATATGATCGAATGAAGAT 124
DB 152 TCAGAAATCATGGGTGAGGTGAGAAATGCGGGTTCCTTCTTCCAGAAATCGGAA 211
QY 125 CATGATATGGAAGACGAGCCCGCATTTGATTCGGGCGCAATTCCTCGTTAAGTGAATCTTAAAG 184
DB 212 ACCGACACCAAAAGCGTGGCGGTGCGGAGAAACCGCCTTCTCGGTGGGAGATCTGAAG 271
QY 185 AAAGCAATCCCTGCAATTCGCTTCGGCGGATCCGCGCTCTGCTCATCTCTGCTACGTAGTT 244
DB 272 AAAGCAATCCCGCGCATTTGTTTCAAAGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 331
QY 245 CAGGATCTCATTTATCACCTTCCTTTTATACAGGTGCGCAACACCTACATTTCTCTACCTC 304
DB 332 AGTGACATCATTTATAGCCTCATGCTTCTACTACGTGCGCAACCAATTTACTTCTCTCTC 391
QY 305 CTTCTCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTTTGGCAATCTTGGCATCTC 364
DB 392 CTTCAAGCTCTCTCTTACTTGGCTTGGCCACTCTATTTGGGCCCTGTCAAGCTGTGTCTTA 451
QY 365 ACTGGTTTATGGTCTCTCGGCCATGAATCGCGCCCATCATGCTCTTTAGTAGTACCAAGTG 424
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452 ACTGGTATCTGGTTCATAGCCACGAATGGCGTACACGCACTTACGCGACTACCAATGG 511
425 ATTGATAACGGCGTTGGATTCGTCTCCATTCGGGTCTCTCCACCCCTTACTTTTCTGG 484
512 CTGGATGACACAGTTGGTCTTATCTTCCATTCCTCTCTCTCTCTCTCTCTCTCTCT 571
485 AAATACAGCCATCGAAACACCATGCAACAAATTCACCTCGAAAGAGAGAGTTTAC 544
572 AAGTATAGTATCGCGGTACCAATTCACCACTGGATCCCTCGAAAGAGATGAAGTATTT 631
545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACG 604
632 GTCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACACCT 685
605 CTGGTCAAGTCTCATCTTGGTCAATCATGTTAACTTGAATTTCTTGAATTTCTTTA 664
686 CTGGACGCATCATGATGTTAAACCGTCCAGTTTGTCTCGGTGGCCCTTGTACTTAGCC 745
665 ACGAATGTTTCAGGCAAGAGTACGATAGATTACCAACCACTTTGATCCATTGAGCCG 724
746 TTTAAACGCTCTCGGCAGACCGTATGACGGGTTGCTTGCCTATTTCTCCCAACGCTCCC 805
725 ATCTTCACCGCGTGGAGCAATCAGGTTCGGTTTATCAGATCTTGGTATCGTTCGAGTG 784
806 ATCTAATATGACCGAGAGCGCTCCAGATATACCTCTCTGATCGGGTATTTAGCCGTC 865
785 TTTTACGAGCTCAAGTTCTTGTGTACAAACAAAGAGATTTGGTGGGTGATGTCATGAT 844
866 TGTTTTGGTCTTTACCGTTACGCTGCTGCACAAAGGATGGCTCGATGATCTGCCCTTAC 925
845 GGAGTTCCAGTATAGTCTGAAATTCCTTATTCATTCGTTAATCACTTATCTGCACACACA 904
926 GGAGTACCGCTTCTGATAGTGAATGCGTTCCTCTGCTTGTATCAGTCTTGGAGCACT 985
905 CATCTGTGCTCACCCTATTAAGATTCAACCGAATGGAATCGAATCGAATCGAATCGAAT 964
986 CATCCCTGTTGGCTCCTACTACGATTCATCAGATGGGACTGGCTCAGGGAGCTTTGGCT 1045
965 ACAATCGACAGAGATTTCCGTTCTCTGATCGGATCGGTTTTCACGAGCTTTACACACCC 1024
1046 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGTGTTCACAAATTTACAGACACAC 1105
1025 GTGTTGACCATTTGTTTCCCTACATTCACATTCATGCAAGGAGGCAAGCGAGGCC 1084
1106 GTGGCTCATCACTGTTCTCGCAATGCGCATTAACGCAATGGAAGCTCAAAAGCGG 1165
1085 ATCAAGCCAACTCTGGGTGATTACAGGATGATCGACAGGACTTCCATTTTCAAAGCAATG 1144
1166 ATAAAGCCAACTCTGGGAGACTTTACCAAGTTTCGATGGAAACACCGTGTATGTAGCGATG 1225
1145 TGGAGAGGCGCAAGAAATGCAATTTACATCGAGCAAGATGCAAGCAGCAAGCAAAAGG 1204
1226 TATAGGGAGGCAAGAGAGTATCTATGTAGAACCGGACAGGGAAGGTGACAAGAAAGGT 1285
1205 ACATATTGGTACCAATAAATGTAAT 1229
1286 GTGTACTGGTACAAATAAAGTTAT 1310

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RESULT 7

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US-11-056-355B-109784
; Sequence 109784, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190

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; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109784
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1459)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
; OTHER INFORMATION: as cited in SEQ ID NO 52711
; US-11-056-355B-109784

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Query Match      30.3%; Score 426.2; DB 9; Length 1459;
Best Local Similarity 61.0%; Pred. No. 7.5e-82;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

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QY 65 TTCAGAAATCTGGAGAGGTAGCAGAAATGTCGGAATTCATATGATGATCGAATGAAGAT 124
Db 152 TCCAGAAACATGGGTGCGAGGTGGAAGAAATGCGGTTCCTACTTCTTCCAGAAATCGAA 211
QY 125 CATGATATGACGAAACAGAGCCCGATTTGATCCGGGCGCATTCCTGTTAAGTGATCTAAAG 184
Db 212 ACCGACACCAAAAGCGTGTGCGGAGAAACCGGCTTCTCGGTGGGAGATCTGAAG 271
QY 185 AAAGCAATCCCTGCACATTTGCTCCGGCGATCCCGCTCTGGTTCATCTCTGCTAGTAGTT 244
Db 272 AAAGCAATCCCGCGCATTTGTTCAAGCGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 331
QY 245 CAGATCTCATTTATCACCTTCTTTTATACAGGTGCGCAACACCTACATTCCTCACCTC 304
Db 332 AGTGACATCATTTATAGCTCTATGCTTCTACTACGTGCGCAACCAATTAATCTCTCTCTC 391
QY 305 CCTCCTCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTTCGCAATCTTGCATCTC 364
Db 392 CCTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTCTCAAGGCTGTGCTCTA 451
QY 365 ACTGGTTTATGGGCTCTCGGCATGAATGGCGCATCATGCTTTTAGTAGTACAGTGG 424
Db 452 ACTGATCTGGGTTCATAGCCACGAATGGGTCCACGCAATTCAGCGACTTACCAATGG 511
QY 425 ATTGATAACGGCGTTGGATTCGTCTCTCATTTCCGCTCTCTCACCCCTTACTTTTCTGG 484
Db 512 CTGGATGACACAGTTGGTCTTATCTTCCATTTCTTCTCTCTCTCTCTCTCTCTCTGG 571
QY 485 AAATACAGCCATCGAAAGCAGCAATGCAAAACAAATTCACCTCGAAAGAGAGAGTTTAC 544
Db 572 AAGTATAGTATCGCGGTACCAATTCCAACACTGGATCCCTCGAAAGAGATGAAGTATTT 631
QY 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACG 604
Db 632 GTCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACACCT 685
QY 605 CTGGTCAAGTCTCATCTTGGTCAATCATGTTAACTTGAATTTCTTGAATTTCTTTA 664
Db 686 CTGGACGCATCATGATGTTAAACCGTCCAGTTTGTCTCGGTGGCCCTTGTACTTAGCC 745
QY 665 ACGAATGTTTCAGGCAAGAGTACGATAGATTACCAACCACTTTGATCCATTGAGCCG 724
Db 746 TTTAAACGCTCTCGGCAGACCGTATGACGGGTTGCTTGCCTATTTCTCCCAACGCTCCC 805
QY 725 ATCTTCACCGCGTGGAGCAATCAGGTTCGGTTTATCAGATCTTGGTATCGTTCGAGTG 784
Db 806 ATCTAATATGACCGAGAGCGCTCCAGATATACCTCTCTGATCGGGTATTTAGCCGTC 865
QY 785 TTTTACGAGCTCAAGTTCTTGTGTACAAACAAAGAGATTTGGTGGGTGATGTCATGAT 844
Db 866 TGTTTTGGTCTTTACCGTTACGCTGCTGCACAAAGGATGGCTCGATGATCTGCCCTTAC 925

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QY 845 GGAGTTCCAGTGTGATGAGTCTGAATTCCTTCAATATCGTAATCACTTATCTGACACACACA 904  
|||||  
Db 926 GGAGTACCGCTTCTGATAGTGAATGCGTCTCTGATCACTTACTTGCAGCACACT 985  
QY 905 CATCTGTCTGACCCCATACGATTCACCGAATGGAATGGATCAAGAGCGCTTGACC 964  
Db 986 CATCCCTCTGTGCTCCTCACTACGATTCATAGAGTGGAGTGGCTCAGGAGAGCTTGGCT 1045  
QY 965 ACAATCGACAGAGATTCGGTCTCTGAAATCGGGTTTCCACGAGCTTACACACCCAC 1024  
Db 1046 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACAAATTAACAGACACAC 1105  
QY 1025 GTGTTGCCACATTTGTTCCCTACATTCACATTAATCATGCAAGAGGCAAGCGAGGCC 1084  
Db 1106 GTGGCTCATCCCTGTCTCGCAATGCGGCATTTAAGCAATGGAAGCTACAAGGGG 1165  
QY 1085 ATCAAGCCCAATCTTGGTGATTAACAGGATGATCGACGAGCTCCATTTTCAAAGCAATG 1144  
Db 1166 ATAAAGCCCAATCTGGGAGACTATTAACAGTTGATGGAAACCGTGGTATGTAGCGATG 1225  
QY 1145 TGGAGAGAGCGCAAGGAATGCAATTTACATCGAGCAAGATGCGACAGCAAGCAAAAGG 1204  
Db 1226 TATAGGAGCGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1285  
QY 1205 ACATATGTGTACCATTAATATGTAAT 1229  
Db 1286 GTGTACTGTGTACAAATAAGTTAT 1310

## RESULT 8

US-10-547-086-17  
; Sequence 17, Application US/10547086  
; Publication No. US20060195919A1  
; GENERAL INFORMATION:  
; APPLICANT: CropDesign N.V.  
; TITLE OF INVENTION: Arabidopsis promoters  
; FILE REFERENCE: CD-075-PCT  
; CURRENT APPLICATION NUMBER: US/10/547,086  
; CURRENT FILING DATE: 2005-08-26  
; PRIOR APPLICATION NUMBER: EP 03075587.0  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 17  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: TC160765 (PRO0193)  
US-10-547-086-17

Query Match 30.3%; Score 426.2; DB 6; Length 1617;  
Best Local Similarity 61.0%; Pred. No. 7.7e-82;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;  
QY 65 TTTCAGAAATCTGGGAGAGTAGCAGAAATGTCGATTCATATGATGATCGAATGAAAGAT 124  
Db 149 TCAGAAACATGGGTGAGGTGGAAGATGCCGGTTCCTACTTCTTCCAGAAATCGGAA 208  
QY 125 CATGATATGGACGAACAGAGCCCGATTTGATCCGGGCCATTCCTGTTAAAGTATCTTAAAG 184  
Db 209 ACCGACACCAAAAGCGTGTGGCGTGGAGAAACCGCCCTTCTCGGTGGAGATCTGAAG 268  
QY 185 AAAGCAATCCCTGACATGCTTCCGGCGATCCGCGCTGTGTCATCTCTGCTACGTAGT 244  
Db 269 AAAGCAATCCCGCGATTTGTTTCAACCGCTCAATCCCTCGCTCTTCTCTACCTTATC 328  
QY 245 CAGGATCTCATATATCACTTCTTTTATACAGCTGCGCAACACCTTACATTTCTCACCTC 304  
Db 329 AGTGACATATATAGCCTCATGCTTCTACTAGTCGCCACCAATTAATTTCTCTCTCTC 388  
QY 305 CCTCCTCTCTAGTTTACTTAGCATGGCGGTTTACTGGTTTTTGCCTTGTGCAATCTTGCATCCTC 364

## RESULT 9

US-11-056-355B-75573  
; Sequence 75573, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby

Db 399 CCTCAGCCTCTCTCTTACTTGGCCACTCTATTTGGGCTCTGTCAGAGCTGTGTCTTA 448  
QY 365 ACTGCTTTATGGGTCTCGGCCATGAATGCGGCCATCATGCTCTTTAGTGAGTACCAAGTG 424  
Db 449 ACTGCTATCTGGTCTATAGCCCAACCAATGCGGTACCAAGCATTCAGCGACTACCAATG 508  
QY 425 ATTGATAACGCCGTTGGATTTGTCCTCATTTGGGTCTCTCTCACCCCTTACTTTTCTTGG 484  
Db 509 CTGGATGACACAGTTGGTCTTATCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTCT 568  
QY 485 AAATACAGCCATCGAAACACCAATTCACATTCACATTCACATTCACATTCACATTCAC 544  
Db 569 AAGTATAGTATGTCGCGCTCACCATTTCCACACTGGATCTCTCGAAAGAGATGAAGTAT 628  
QY 545 ATTCTCTAGAACTCAGTCTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAA 604  
Db 629 GTCCCAAGACGAAATCAGCAATCAAGTGGTACGGGAATATC-----CTCAACAA 682  
QY 605 CTGCTGCAATCCTCATCTTGGTCAATCATGTTAACTTGAAGATTTCTTATACCTTTTA 664  
Db 683 CTGAGCGCATCATGATGTTAACTGTTGCTCGGGTGGCCCTTGTACTTATAGCC 742  
QY 665 ACGAATGTTTCAGGCAAGAGTACGATAGATTTTCAACCACTTTGATCCATTTGAGCCG 724  
Db 743 TTTAAGCTCTCTGGCAGACCGTATGCGGTTCGGTTCGCTTCTTCCCAACCGTCTCC 802  
QY 725 ATCTTTCACGCGGTGAGCGAATCCAGGTTCGGTTTATCAGATCTTGGTATCTTGCAGTG 784  
Db 803 ATCTAATATGACCGAGAGCGCTCCAGATATACCTCTCTGATGCGGTATTTCTAGCCG 862  
QY 785 TTTTACGACTCAAGTTCTTGTGTAACAAACAAAGATTTGGTGGGTGATGTCATGTAT 844  
Db 863 TGTCTTGGTCTTTACCGTTACGCTCTGCAAGGGATGGCCCTCGATGATCTGCTCTTAC 922  
QY 845 GGAGTTCAGTGATAGTCTGAAATTCCTTCAATTCGTAATCACTTATCTGACACACACA 904  
Db 923 GGAGTACCGCTTCTGATAGTGAATGCTTCTCTGCTTGTGATCACTTACTTGCAGCAC 982  
QY 905 CATCTGTCTCACCCCATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 964  
Db 983 CATCTCTGTTGCTCTCACTACGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1042  
QY 965 ACAATCGACAGAGATTTCCGTTCTCTGAAATCGGGTTTCCACGAGTTTACACACCCAC 1024  
Db 1043 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACAACTTACAGACAC 1102  
QY 1025 GTGTTGACCAATTTGTTTCCCTACATTCACATTCATCATGCAAGAGGCAAGCGAGCC 1084  
Db 1103 GTGGCTCATCACTCTTCTCGCAATGCGCAATTAACGCAATGGAAGCTACAAGGGC 1162  
QY 1085 ATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACGAGCTCCATTTTCAAAGCA 1144  
Db 1163 ATAAAGCAATTTCTGGGAGACTTATTCAGATTCGATGGAACCGTGGTATGTAGCGATG 1222  
QY 1145 TGGAGAGAGCGCAAGGAATGCAATTTTATCTGAGCAAGATGCAAGAGCAAGCAAGGG 1204  
Db 1223 TATAGGAGGCAAGAGAGTGTATCTATGTAGAACCGGACAGGGAAGGTGCAAGAAAG 1282  
QY 1205 ACATATGTTGGTACCAATAAATGTAAT 1229  
Db 1283 GTGTACTGTGTACAAATAAGTTAT 1307

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; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 75573
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1389)
; OTHER INFORMATION: Ceres Seq. ID no. 6444000
;
; Query Match      30.2%; Score 425.2; DB 9; Length 1389;
; Best Local Similarity 61.0%; Pred. No. 1.2e-81;
; Matches 710; Conservative 0; Mismatches 448; Indels 6; Gaps 1;
;
QY 66 TCAGAAATCTGGAGAGGTAGCAGAAATGTGGATTATATGATGATCGAATGAAGATC 125
Db 130 TCTGAAATCTGGGTGAGGTGGAAGAAATGCCGGTTCCTACTTCTTCCAGAAATCGGAAA 189
QY 126 ATGATATGAGCAACGAGCCCGATTGATCCGGCCCAATCTCGTTAAGTGTATTAAGA 185
Db 190 CCGACACCAAGAGCGTGTCCGTCGGAGAAACCCGCTTCTCGTGGAGATCTGAAGA 249
QY 186 AAGCAATCCCTGCACATTTCTCCGGCGATCGCGCTGTGGTCACTCTGCTACGTAGTTC 245
Db 250 AAGCAATCCCGCGCATTTGTTCAACGCTCAATCCCTCGCTCTTCTCCTACCTTATCA 309
QY 246 AGGATCTCATATACCTTCTCTTTATACAGGTCGCGCAACACCTTACATTCCTACCTCC 305
Db 310 GTGACATCATATAGCCTCTACTGCTTCTACTAGTCGCGCAACAAATTTCTCTCTCTCC 369
QY 306 CTCCTCTCTAGTTTACTTACATGCGCGGTTTACTGGTTTGGCAATCTTGCACTCCCA 365
Db 370 CTCAGCCTCTCTTACTTTGGCTTGGCCACTCTATTGGGCGCTGTCAAGGCTGTGCTCAA 429
QY 366 CTGGTTTATGGTCTCTCGGCCATGAATGGGCCATCATCGCTTCTTATAGTAGTACCAAGTGA 425
Db 430 CTGGTATCTGGGTATAGCCACAGATGGGTCAACCGCATTCAGCGACTACCAATGGC 489
QY 426 TTGATAACGCCGTGGATTGCTCTCATTTGGCTCTCTCACCCTTACTTTTCTTGGGA 485
Db 490 TGGATGACACAGTTGGTCTTATCTTCCATTTCTTCTCTCTCTCTCTCTCTCTCTCTGGA 549
QY 486 AATACAGCCATCGAAGACACCATGCAACACAAATTCATCGAAGACGAGGAAGTTTACA 545
Db 550 AGTATAGTATCGCGCTCACCATTCCAACATGGATTCCTCGAAGAGATGAAGTATTGG 609
QY 546 TTCTTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACACACGC 605
Db 610 TCCCAAGACAGAAATCAGCAATCAAGTGTGTCAGGGAATAC-----CTCAACACCCCTC 663
QY 606 CTGGTCGAATCTCATCTTTGGTCATCATGTTAACTTAGGATTTCTTTATACCTCTTAA 665
Db 664 TTGGACGCTATGATGTTAAACCGTCCAGTTTGTCTCGGGTGGCCCTTTGACTTAGCCT 723
QY 666 CGAATGTTTTCAGGCAAGATAGATAGATTTACCAACCACTTTTGATCATTGAGCCCGGA 725
Db 724 TTACGCTCTCTGGCAGACCGTATGACGGGTTGCTTGGCATTTCTTCCCAACGCTCCCA 783
QY 726 TCTTCCAGCGAGGTGAGGGAATCCAGGTTTGGCTTATCAGATCTTGGTATCGTTGAGTGT 785
Db 784 TCTACAATGACCGAGAACGCTCCAGATATACCTCTCTGATGCGGGTATTTCTAGCGCT 843
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QY 786 TTTACGGACTCAAGTTTCTTGATCAAAACAAAGGATTGGTTGGTGTGATGTGCGATGATG 845
Db 844 GTTTTGGTCTTTTACCGTTACCGCTCTGCACAAAGGATGGCTCTGATGATCTGCTCTACG 903
QY 846 GAGTTTCCAGTATAGGTCTGAATTCCTTCAATTCGTAAATCACCTTATCTTGACACACAC 905
Db 904 GAGTACCGCTTCTGATAGTGAATCGGTTCTCGTCTTGATCACCTTACTTTGCAGCACACTC 963
QY 906 ATCTGTGTCACCCCATTTACGATTCACCGAATCGAACTGGAATCAAGGAGCCTTGACCA 965
Db 964 ATCCCTCGTTCCTCTCACTTACGATTCATCAGATGGGACTGGCTCAGGGGAGCTTTGGCTA 1023
QY 966 CAATCGACAGAGATTCGGTCTCTGATCGGTTTCCACGAGCTTACACACACCCACG 1025
Db 1024 CCGTAGACAGAGACTTACGGAATCTTGAAACAGGTTGTTCCACACATTTACAGACACACAG 1083
QY 1026 TGTTCACCACTTTTCTTCCCTTACATTTCCACATTTATCATGCAAGGAGGCAAGCGAGGCA 1085
Db 1084 TGGCTCATCACCTCTTCTCGACATCGCCATTTATACGCAATGGAAGCTACAAAGGCGA 1143
QY 1086 TCAAGCCAAATCTTGGGTGATTACAGGATGATCGACAGACTTCCATTTTTCAAAGCAATGT 1145
Db 1144 TAAAGCCAAATCTCGGAGACTTATTACCAAGTTTCGATGGAAACACCGTGGTATGTAGCGATGT 1203
QY 1146 GGACAGAGGCCCAAGGAATGCAATTTACATCGAGCAAGATGCAAGACAGCAACAAAGGGA 1205
Db 1204 ATAGGAGGCAAGAGGTGATCTATGTAGAACCGGACAGGAAGGTGACAAAGAAAGTG 1263
QY 1206 CATATTGGTACCATATAAAATGTAAT 1229
Db 1264 TGTACTGTTACCAACAATAAGTTAT 1287

RESULT 10
US-11-056-355B-42535
; Sequence 42535, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 42535
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1451)
; OTHER INFORMATION: Ceres Seq. ID no. 12337750
;
; NAME/KEY: misc feature
; LOCATION: (1)..(1451)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 15177298
; OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-42535
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Query Match      30.2%; Score 424.6; DB 9; Length 1451;
Best Local Similarity 60.9%; Pred. No. 1.7e-81;
Matches 710; Conservative 0; Mismatches 449; Indels 6; Gaps 1;
;
QY 65 TTCAGAAATCTGGAGAGGTAGCAGATGTCCGATTTCATATGATGATCGATGAAGAT 124
Db 144 TCCAGAAACATGGGTGCGAGGTGGAAGATGCCGTTCTCTTCTTCCAGAAATCGGAA 203
QY 125 CATGATATGGACGAAACGAGCCCGATTTGATCCGCGCGCATTTCTCGTTAAGTGATCTAAAG 184
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Db 204 ACCGACACCAAGCGTGTGCGTGCAGAAACCGCCTTTCTCGGTGGGAGATCTGAAG 263  
Qy 185 AAAGCAATCCCTGCAATGCTTCCGGCGATCGCGCTCTGCTCATCTCTGCTACGTAGTT 244  
Db 264 AAAGCAATCCGGCGATGTTTCAACGCTCAATCCCTCGCTCTTCTCTACCTTATC 323  
Qy 245 CAGGATCTCATATATCACTTCTCTTTTATACAGGTGCGCAACACCTTACATCTCTCACTC 304  
Db 324 AGTGACATCATATAGCTCATGCTTCTACTAGTGCAGCAAAATTACTTCTCTCTCTC 383  
Qy 305 CTTCTCTCTCTAGTTTACTAGATGCGCGGTTTACTGTTTGTGCAATCTTGCATCTC 364  
Db 384 CTTGACCTCTCTCTTACTTGGCTTGGCCACTATTTGGGCTGTCAAGGCTGTGTCTTA 443  
Qy 365 ACTGGTTTATGGTCTCTCGGCCATGAATGGGCCATCATGCTCTTTAGTGAGTACAGTGG 424  
Db 444 ACTGGTATCTGGTCTATAGCCACGAATGGGTACCAACGCAATTCAGCGACTACCAATGG 503  
Qy 425 ATTGATAACGCGGTTGGATTGCTCTCAATTCGGCTCTCTCAACCCCTTACTTTTCTGG 484  
Db 504 CTGGATGACACAGTTGGTCTTATCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTGG 563  
Qy 485 AAATACAGCCATCGAAAGCACCATGCARACAAATTTCACTCGAAACGAGGAAGTTTAC 544  
Db 564 AAGTATAGTCATCGCGCTCACCAATCCAACTGGATCCCTCGAAAGATGAAGTATTT 623  
Qy 545 ATTCTTAGAACTCAGTCCCGCTCAGACTTACTCCACATACGAATTTCTTGACACAGG 604  
Db 624 GTCCCAAGAGCAATCAGCAATCAAGTGTAGCGGAATAC-----CTCAACACCT 677  
Qy 605 CTGTGTCGAATCTCATCTTGTGTCATCTGTTAACTTGAAGTTTCTTTTATACCTTTA 664  
Db 678 CTTGAGCGCATCATGATGTTTAACTGCTTGTCTCGGGTGGCCCTTGTACTTAGCG 737  
Qy 665 ACGAATGTTTCAGGCAAGATGATAGATTTACCAACCACTTTCATTCATTTGAGCCCG 724  
Db 738 TTTAAGCTCTCTGCGACACGATGATGCGGTTGCTTGGCCATTTCTTCCCAACGCTCC 797  
Qy 725 ATCTTCAACGAGGCTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGCACTG 784  
Db 798 ATCTAATAGCCAGAAAGCCTCCAGATATACCTCTCTGATGCGGGTATTTAGCCGTC 857  
Qy 785 TTTTACGCACTCAAGTTCTCTGTACAAACAAAGAAATTTGGTTGGTGTATGTCATGTAT 844  
Db 858 TGTGTTGGTCTTTACGCTGCTGCAAGGATGCGCTCGATGATCTGCTCTAC 917  
Qy 845 GGAGTTCCAGTAGGTCTGAATCTCTTCAATTCATTCATCTTATCTGACACACACA 904  
Db 918 GGAGTACCGGTTCTGATAGTGAATGCGTTCTCTGCTTGTATCACTTACTTGCAGCACT 977  
Qy 905 CATCTGCTCAACCCATTAAGATTCACCGAATGGAATGGATCAAGAGGCTTGACC 964  
Db 978 CATCCCTGCTGCTCACTACGATTCATCAGAGTGGACTGGCTCAGGGAGCTTTGGCT 1037  
Qy 965 ACAATCGACAGAGATTTCGCTCTCTGAATTCGGGTTTTCACGACGTTTACACACCCAC 1024  
Db 1038 ACGTAGACAGAGACTACGGAATCTTGAACAAGGTTTCCACAACATTTACAGACACAC 1097  
Qy 1025 GTGTTGCAACATTTGTTTCCCTACATTCACATTCATCATGCAAGAGGCAAGGAGGCC 1084  
Db 1098 GTGGCTCATCACCTGTTCTCGAACAATCCGCAATATATAAGCAATGGAAGCTACAAAGGG 1157  
Qy 1085 ATCAAGCCATCTTGGGTGATTAAGGATGATCGACGAGCTCCATTTTCAAGCAATG 1144  
Db 1158 ATAAAGCCAAATCTGGGAGACTATTAACAGTTTCATGGAACAACCGTGTATGTTGGGATG 1217  
Qy 1145 TGGAGAGAGCCCAAGGAATTCATTCATCGACCAAGATGCAACAGCAAGCAAGAGG 1204  
Db 1218 TATAGGAGGCAAGAGGTATCTATGTAGAACCCGACAGGGAAGGTGACAGAGGT 1277  
Qy 1205 ACATATTGGTACATAAATGTAAAT 1229  
Db 1278 GTGTACTGGTACAAACAATAGTTAT 1302

RESULT 11  
US-11-056-355B-28874  
; Sequence 28874, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 28874  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1411)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298  
; OTHER INFORMATION: as cited in SEQ ID NO 52711  
US-11-056-355B-28874

Query Match 30.1%; Score 423; DB 9; Length 1411;  
Best Local Similarity 60.9%; Pred. No. 3.6e-81;  
Matches 709; Conservative 0; Mismatches 450; Indels 6; Gaps 1;  
Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGATGTGCGGATTCATATGATGATCGAATGAAGAT 124  
Db 152 TCCAGAAACATGGTGCAGGTGGAAGATGCGGTTCCTACTTCTTCCAGAAATCGGAA 211  
Qy 125 CATGATATGACGACGAGCCCGATTTGATCGGCGCATCTCGTAAAGTATCTTAAAG 184  
Db 212 ACCGACACCAAAAGCGTGTGCGGTGCGAGAAACCGCTTCTCGGTGGAGATCTGAAG 271  
Qy 185 AAAGCAATCCCTGCAATGCTTCCGGGATCCGCGCTCTGCTCATCTCTGCTACGTAGTT 244  
Db 272 AAAGCAATCCCGCGCATGTTTCAACGCTCAATCCCTCGCTCTTCTCTACCTTATC 331  
Qy 245 CAGGATCTCATATCACTTCTCTTTTATACAGGTGCGCAACACCTTACATTCCTCACTC 304  
Db 332 AGTGACATCATATAGCTCATGCTTCTACTACGTGCGCACCAATTACTTCTCTCTCTC 391  
Qy 305 CTTCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCAATCTTGCATCTCTC 364  
Db 392 CCTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTTGGGCTGTCAAGGCTGTGCTTA 451  
Qy 365 ACTGGTTTATGGTCTCTCGCCATGAATGCGGCCATCATGCTCTTGTAGTGAGTACAGTGG 424  
Db 452 ACTGGTATCTGGTCTATAGCCCAAGATGCGGTACCAGCATTCAGCGACTACCAATGG 511  
Qy 425 ATTGATAACGCGGTTGGATTCTCTCAATTCGGGTCTCTCACTCGGCTTCTTCTTCTGG 484  
Db 512 CTGGATGACACAGTTGGTCTTATCTTCCATCTCTCTCTCTCTCTCTCTCTCTCTGG 571  
Qy 485 AAATACAGCCATCGAAAGCACCATCGAAACAAATTCATCTGAAACGAGGAAGTTTAC 544  
Db 572 AAGTATAGTCATCGCGCTCACCAATTCGAATCCCTCGAAAGATGAAGTATTT 631  
Qy 545 ATTCTTAGAACTCAGTCCCGCTCAGGACTTACTCCACATCAGGAATTTCTTGACACAG 604  
Db 632 GTCCCAAGCAAGATCAGCAATCAAGTGTAGCGGAATAC-----CTCAACACCT 685  
Qy 605 CTTGTCGAATCTCATCTTGGTTCATGTTAACTTAGGATTTCTTTTATACCTCTTA 664



Db 686 CTGACGCATCATGATGTTAAACGTCAGTTTGTCTCGGGTGGCCCTTGATCTAGCC 745  
Qy 665 ACGAATGTTTTCAGGCAAGAGTACGATAGATTACCAACCACTTTGATPCCATTGAGCCG 724  
Db 746 TTTAAAGCTCTCTGGCAGACCGTATGACGGTTGCGTTGCCATTCTTCCCAACGCTCC 805  
Qy 725 ATCTTACCGAGCGGTGAGCAATCCAGGTGGGTATCAGATCTTGGTATCGTTGCGAGTG 784  
Db 806 ATCTACAATGACCGAAGACGCTCCAGATATACCTCTCTGATGCGGGTATTTCTAGCCGTC 865  
Qy 785 TTTTACGACCTCAAGTTTCTGTACAAACAAAGGATTTGGTGGTGATGCGATGAT 844  
Db 866 TGTTTGTGCTTTACCGTTACGCTGCTGCACAAGGATGGCCTCGATGATCTGCCCTCTAC 925  
Qy 845 GGAGTTCAGTGATAGGTCTGAATTCCTTTATATCGTAAATCACTTATCTGCACCAACA 904  
Db 926 GGAGTACCGCTTCTGATAGTGAATGCGTTCTCGTCTTGATCACTTACTTGCAGCACT 985  
Qy 905 CATCTGCTGACCCCATTTAGATTCAACCGAATGGAATCGATCGAATCAAGAGCGCTTACC 964  
Db 986 CATCCCTGTTGCCCTCACTACGATTCATCAGATGGGACTGGCTCAGGGGAGCTTTGGCT 1045  
Qy 965 ACAATCGACAGATTTTCGGTCTCTGATCGGTTTCCAGAGTTTACACACACCCAC 1024  
Db 1046 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACAACATTACAGACACAC 1105  
Qy 1025 GTGTTGACCAATTTGTTTCCCTACATTCACATTAATATGATCAAGAGGCAAGCGGCC 1084  
Db 1106 GTGGCTCATACCTGTTCTCGCAATGCGCATTAAGCAATGGAAGCTTACAAATGCG 1165  
Qy 1085 ATCAAGCCAAATCTTGGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATG 1144  
Db 1166 ATAAAGCCAAATCTGGGAGACTATTACCAGTTTCGATGGAACACCGTGTATGTGGCATG 1225  
Qy 1145 TGGAGAGGCGCAAGGATGATTTACATCGAGCAAGATGACAGCAGCAAGCAAGAGG 1204  
Db 1226 TATAGGGAGGCAAGGATGATTTATGTAGAACCGGACAGGAGGTGACAAAGAGGT 1285  
Qy 1205 ACATATGCTTACCATAAAATGTAAT 1229  
Db 1286 GTGACTGTACACAAATAGTTAT 1310

## RESULT 12

US-11-056-32464  
; Sequence 32464, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590RUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 32464  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1411)  
; OTHER INFORMATION: Ceres Seq. ID no. 12321215  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1411)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298  
; OTHER INFORMATION: as cited in SEQ ID NO 52711  
; US-11-056-32464

Query Match 30.1%; Score 423; DB 9; Length 1411;  
Best Local Similarity 60.9%; Pred. No. 3.6e-81;  
Matches 709; Conservative 0; Mismatches 450; Indels 6; Gaps 1;  
Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTTCATATGATGATCGAATGAAAGAT 124  
Db 152 TCCAGAAACATGGGTGAGGTGGAGAAATGCGGTTCCTACTTCTTCCAGAAATCGAA 211  
Qy 125 CATGATATGACGAAACGAGCCCGGATTTGATCCGGCGCATTTCTGGTTAAGTATCTAAAG 184  
Db 212 ACCGACACCAAAAGCGTGTGGCGTGAGAAACCGCTTCTCGGTGGAGAGTCTGAAG 271  
Qy 185 AAAGCAATCCCTGACATATTGTTCCGGGATCGCGCTCTGGTCTGATCTCTGCTAGTATT 244  
Db 272 AAAGCAATCCGGCGCATTTGTTCAAACGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 331  
Qy 245 CAGGATCTCATTTATCACCTTCTTTTATACAGGTGCGCAACACCTACATTCCTCACCTC 304  
Db 332 AGTGACATCATTTAGCTCATGCTTCTACTAGTCCGCCAACCAATTTACTTCTCTCTCTC 391  
Qy 305 CTTCTCTCTCTAGTTTACTTATGACATGCGCGTTTACTGGTTTGGCCAACTTTGCAATCTC 364  
Db 392 CTTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGCTTA 451  
Qy 365 ACTGGTTTATGGGTCTCGGCCATGAATGCGGCATCATGCTTTAGTGTAGTACAGTGG 424  
Db 452 ACTGGTATCTGGGTCAATGAGCCAGAAATGCGGTGACCAACGCAATTCAGCGCATACCAATGG 511  
Qy 425 ATTGATAAGCGCGTTGGATTGCTCTCCATTTGGCTCTCTGCTCACCCCTTACTTTCTTGG 484  
Db 512 CTGATGACACAGTTGGTCTTATCTTCCATTTCTTCTCTCTCTCTCTCTCTCTCTCTCT 571  
Qy 485 AAATACAGCCATCGAAAGCACCATGCAAAACACAAATTCATTCGAAAAACGAGGAATTTAC 544  
Db 572 AAGTATAGTCATCGCGCTCACCATTCCAAACACTGGATCCCTCGAAAGAGATGAAGTATTT 631  
Qy 545 ATTCCTAGAACTCAGTCCGAGCTCAGCACTTCTCCACATACGAATTTCTTGACAAACAG 604  
Db 632 GTCCAAAGCAGAAATCAGCAATCAAGTGTGACGGAAATAC-----CTCAAACAGCCCT 685  
Qy 605 CTTGGTGGAAATCCTCATCTTGGTTCATCATGTTAACTTAGGATTTCTTTATACCTCTTA 664  
Db 686 CTTGGACGCATCATGTTTAAACCGTCAAGTTTGTCTCTCGGTGGCTTGTACTTATGACC 745  
Qy 665 ACGAATGTTTTCAGCAAGAGTACGATAGATTTTACCAACCACTTTGATTCATTCAGCCGC 724  
Db 746 TTTAAAGCTCTCTGGCAGACCGTATGACGGGTTCGCTTGGCCATTTCTTCCCAAGGCTCCC 805  
Qy 725 ATCTTACCGAGCGGTGAGCGAATCCAGGTTCGTTATCAGATCTTGGTATCGTTGCAAGTG 784  
Db 806 ATCTACAATGACCGAAGACGCTCCAGATATACCTCTCTGATGCGGGTATTTCTAGCCGTC 865  
Qy 785 TTTTACGAGCTCAAGTTTCTTGTACAAACAAAGGATTTGGTGGGTGATGCGATGAT 844  
Db 866 TGTTTGTGCTTTACCGTTACGCTGCTGCACAAGGATGGCCTCGATGATCTGCTCTTAC 925  
Qy 845 GGAGTTCAGTGTAGGTCTGAAATTCCTTATTCGTAATCACTTATCTGACCAACACACA 904  
Db 926 GGAGTACCGCTTCTGATAGTGAATGCGTTCCTCGTCTTGATCACTTACTTGCAGCACT 985  
Qy 905 CATCTGCTGACCCCATTTAGGATTCACCGAATGGAAGTGGATCAAGAGGCGCTTGACC 964  
Db 986 CATCCCTGTTGCCCTCACTACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCT 1045  
Qy 965 ACAATCGACAGAGATTTTCGGTCTCTCGAATCGGGTTTCCACAGCTTTACACACACCCAC 1024  
Db 1046 ACCGTAGACAGAGACTAGGAAATCTTGAACAAAGGTGTTCCACAACATTACAGACACAC 1105  
Qy 1025 GTGTTGACCAATTTGTTTCCCTACATTCACATTTATCATGCAAGAGGCAAGGAGGCC 1084  
Db 1106 GTGGCTCATACCTGTTCTCGCAATGCGCATTAAGCAATGGAAGCTTACAAATGCG 1165





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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/340,318
; FILING DATE: 26-JAN-2006
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,608
; FILING DATE: 08-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,650
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lundquist, Ronald C.
; REGISTRATION NUMBER: 37,875
; REFERENCE/DOCKET NUMBER: 07148/042002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/335-5070
; TELEFAX: 612/288-9696
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
; FEATURE:
; OTHER INFORMATION: Wild type F form.
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; US-11-340-318-1
;
; Query Match      28.6%; Score 402.2; DB 8; Length 1155;
; Best Local Similarity 60.4%; Pred. No. 9,7e-77;
; Matches 700; Conservative 0; Mismatches 449; Indels 9; Gaps 2;
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; DB 2 TGGGTGCAGGTGGAGAAATGCAAGTGTCTCTCCCTCCCAAGAAAGTCTGAAACCGACACCA 61
; QY 135 ACGAAGCGGCCGATGATCGGGCGCATCTCTGTAAGTGATCTTAAGAAAGCAATCC 194
; DB 62 TCAAGCGCGTACCTGCGAGACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATCC 121
; QY 195 CTGCACATTCCTCCGGCGATCCGGCGTCTGGTCACTCTGCTACCTGCTACGATGTCAGGATCTCA 254
; DB 122 CACCGCATGTTTCAACCGCTGATCCCTCGCTCTTCTCTACCTCATCTGGGACATCA 181
; QY 255 TTATCACCCTCTTTTATACACGGTTCGCAACACCTACATTCCTCACTCCCTCTCTCTC 314
; DB 182 TCATAGCTCTCTGCTTCTACTACNTCGCCACCACTTACTTCTCTCTCTCTCTCCTCACCCTC 241
; QY 315 TAGTTTACTAGCATGGCGGTTTACTGGTTTGGCAATCTGCATCTCTCACTGGTTTAT 374
; DB 242 TCTCTACTTCTGCTGCTCTCTACTGGCTGCAAGGGTGTCTTAACCGCGCT 301
; QY 375 GGGTCTCGGCATGAATGCGGCCATCATGCTTCTAGTGAGTACAGTGGATGATGAACG 434
; DB 302 GGGTCATAGCCACGATGCGGCCACCAAGCTTTCAGCGACTACCAAGTGGCTTGACGACA 361
; QY 435 CGGTTGGATTCGCTCTCCATTCGGCTCTCTCAACCCCTTATCTTTCTTGGAAATACAGCC 494
; DB 362 CGGTGGGTCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 421
; QY 495 ATCGAAGCACCATTGCAACACAAATTCATCGAAGACGAGGAAGTTTACATTCCTAGNA 554
; DB 422 ATCGCAGCACCATTTCACAACTGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 481
; QY 555 CTCAGTCCAGCTCAGGACTTACTCCATACATGAAATTTCTGACAAACAGCGCTGGTCGAA 614
; DB 482 AGAAGTCAGACATCAAGTGGTACGGCAAGTAC-----CTCAACAACCCCTTTGGGACGCA 535
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QY 615 TCCTCATCTTGGTTCATCATGTTAACCTTAGAATTTCTCTTATACCTCTTAACGAATGTTT 674
DB 536 CCGTGATGTTAAACGGTTTCAGTTCACTCTCGCTGGCGTTGTACTTAGCCCTTCAACGCT 595
QY 675 CAGCAAGAAGTACGA--TAGATTTTACCAACCACTTTTGATTCATTTGAGCCCGCATCTTCA 731
DB 596 CGGGAAGACCTTAGCAGCGGGCTTCGGTTGCCATTTCCACCCCAACGCTCCCATCTACA 655
QY 732 CCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCTGTTGCGAGTGTTCAG 791
DB 656 ACGACCGCGAGCGTCTCCAGATATACATCTCCGACGCTGGCATCTCTCGCGCTCTGCTACG 715
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DB 716 GTCTCTTCCGTTACGCCCGCGGAGGAGTGGCTCGATGGTCTGCTTCTTACGAGGTCC 775
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DB 776 CGCTTCTGATTGCAATGGTTTCTCTGTTGATCACTTACTTGCAGCACACGATCCTT 835
QY 912 CGTCACCCCATTTACGATTCACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 971
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QY 972 ACAGAGATTTGGTCTCTCGAATCGGGTTTTCACGAGCTTACACACACCCACCTGTTGC 1031
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QY 1032 ACCATTTGTTTCCCTTACATTCACATTTATCATGCAAAAGGAGGCAAGCGGCCATCAAGC 1091
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QY 1092 CAATCTTGGGTGATTAAGAGATGATGACAGGATCTCCATTTTTCAAAGCAATGTGGAG 1151
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; RESULT 15
; US-11-340-318-5
; Sequence 5, Application US/11340318
; Publication No. US20060137040A1
; GENERAL INFORMATION:
; APPLICANT: DeBonte, L. et al.
; TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND
; TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/340,318
; FILING DATE: 26-JAN-2006
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,608
; FILING DATE: 08-AUG-1997
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/675,650  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Lundquist, Ronald C.  
REGISTRATION NUMBER: 37,975  
REFERENCE/DOCKET NUMBER: 07148/042002  
TELEPHONE: 612/335-5070  
TELEFAX: 612/288-9696  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Brassica napus  
FEATURE:  
OTHER INFORMATION: Wild type D form.

US-11-340-318-5

Query Match 28.4%; Score 400; DB 8; Length 1155;  
Best Local Similarity 60.4%; Pred. No. 2.9e-76;  
Matches 699; Conservative 0; Mismatches 450; Indels 9; Gaps 2;

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QY	135	ACGAACGAGCCCGATTGATCGGGCCATTCTCGTTAAGTGTCTAAAGAAAGCAATCC	194
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QY	195	CTGCACATTTGCTTCGGCGATCGCGTCTGTGTCATCTGTCGTCAGTGTTCAGGATCTCA	254
DB	122	CACCGCAGTGTTCAAAGCTCGATCCCTCGCTCTTTCTCTCTAGCTCATCTGGACATCA	181
QY	255	TTATCACCTTCTTTTATACAGGTGCGGCAACACTACATATCTCACTCCCTCCCTCCTC	314
DB	182	TCATAGCCTCTGCTTCTACTAGTCGCGCACCACTTACTTCCCTCTCTCTCCCTCACCC	241
QY	315	TAGTTTACTTAGCAGCGCGGTCTACTGTGTTTGCCAACTTGTGCACTCTCACTGGTTAT	374
DB	242	TCTCTTACTTCGCTTGGCTCTCTACTTGGGCTTGCACGGGCTGCTTAAACGGGCTCT	301
QY	375	GGGTCTCGGCAATGAATCGGCGCATCATGCCCTTTAGTGAGTACCAGTGGATTGATAACG	434
DB	302	GGGTATAGCCACAGAGTGGGCGCACCAAGCTTACGCGACTACCAAGTGGCTGGACGCA	361
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DB	362	CGTGGGCTCATCTTCCACT	421
QY	495	ATCGAAGACCAATGCAACACAAATCTACTCGAAAACGAGGAAGTTTACATTCCTAGAA	554
DB	422	ATCGACGCCACCAATTCACACACTGGCTCTCTCTCGAGAGACGAGAGTGTGTTGCCCA	481
QY	555	CTCAGTCCAGCTCAGGACTTACTCCACATACGAAATTTCTTGACAAACAGCCCTGGT	614
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QY	615	TCCTCATCTTGGTTCATCATGTTAACTTAGGATTTCTCTTTATACCTCTTTAAACGAAT	674
DB	536	CCGTGATGTTAACGGTTTCACTCTCGGCTGGCTTTGTACTTTAGCTTCAACGCTCT	595
QY	675	CAGGCAAGAGTACGA---TAGATTTACCAACCACTTTGATTCATTTGAGCCCGATCTCA	731
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Search completed: September 25, 2006, 00:38:21  
Job time : 304 secs

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Perfect score: 1406  
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Gapop 10\_0 , Gapext 1.0  
Searched: 18892170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 37784340  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

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16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	870	61.9	1364	9	US-10-622-774-9
3	697	49.6	1137	10	US-10-912-534-131
4	681.6	48.5	1134	8	US-10-772-227-27
5	681.6	48.5	1134	10	US-10-912-534-27
6	665.6	47.3	1134	8	US-10-772-227-33
7	665.6	47.3	1134	10	US-10-912-534-33
8	657.8	46.8	1125	8	US-10-772-227-6
9	657.8	46.8	1125	10	US-10-912-534-6
10	657.6	46.8	1309	3	US-09-981-124-3
11	646	45.9	1143	8	US-10-772-227-12
12	646	45.9	1143	10	US-10-912-534-12
13	640.4	45.5	1344	9	US-10-622-774-10
14	640.4	45.5	1358	3	US-09-981-124-1
15	638.6	45.4	1125	8	US-10-772-227-32
16	638.6	45.4	1125	10	US-10-912-534-32
17	611.4	43.5	1199	3	US-09-981-124-19

18	486.4	34.6	1134	8	US-10-772-227-29	Sequence 29, Appl
19	486.4	34.6	1134	10	US-10-912-534-29	Sequence 29, Appl
20	470.6	33.5	1125	10	US-10-912-534-132	Sequence 132, App
21	467.2	33.2	1125	10	US-10-912-534-130	Sequence 130, App
22	467	33.2	6220	7	US-10-176-149-3	Sequence 3, Appli
23	467	33.2	6220	8	US-10-465-800-3	Sequence 3, Appli
24	467	33.2	6220	10	US-10-518-753-3	Sequence 3, Appli
25	462.6	32.9	1586	8	US-10-425-114-14778	Sequence 14778, A
26	462.6	32.9	2931	8	US-10-424-599-123945	Sequence 123945, A
27	459.8	32.7	1457	8	US-10-425-114-12782	Sequence 12782, A
28	430.6	30.6	1152	8	US-10-772-227-7	Sequence 7, Appli
29	430.6	30.6	1152	10	US-10-912-534-7	Sequence 7, Appli
30	430.6	30.6	1541	9	US-10-767-795-1175	Sequence 1175, Ap
31	426.2	30.3	1615	13	US-11-021-666-11	Sequence 11, Appl
32	422.4	30.0	1155	7	US-10-330-775-5	Sequence 5, Appli
33	419.4	29.8	1152	11	US-10-523-503-29	Sequence 29, Appl
34	419.4	29.8	1422	3	US-09-837-751-5	Sequence 5, Appli
35	419.4	29.8	1422	16	US-11-202-731-5	Sequence 5, Appli
36	417.2	29.7	1152	8	US-10-772-227-25	Sequence 25, Appl
37	417.2	29.7	1152	10	US-10-912-534-25	Sequence 25, Appl
38	417.2	29.7	1164	6	US-10-185-578-1	Sequence 1, Appli
39	417.2	29.7	1164	8	US-10-772-227-1	Sequence 1, Appli
40	417.2	29.7	1164	10	US-10-912-534-1	Sequence 1, Appli
41	412.8	29.4	1411	3	US-09-852-399-3	Sequence 3, Appli
42	411	29.2	1164	8	US-10-772-227-30	Sequence 30, Appl
43	411	29.2	1164	10	US-10-912-534-30	Sequence 30, Appl
44	411	29.2	1200	10	US-10-912-534-129	Sequence 129, App
45	407	28.9	2043	9	US-10-739-930-3184	Sequence 3184, Ap

ALIGNMENTS

RESULT 1  
US-10-622-774-1  
; Sequence 1, Application US/106222774  
; Publication NO. US2005002270A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Kentucky Research Foundation  
; APPLICANT: Hildebrand, David  
; APPLICANT: Hatanaka, Tomoko  
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSYGENASE GENE  
; CURRENT APPLICATION NUMBER: US/10/622,774  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 60/396,406  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1406  
; TYPE: DNA  
; ORGANISM: Stokesia laevis  
US-10-622-774-1

Query Match	100.0%;	Score 1406;	DB 9;	Length 1406;
Best Local Similarity	100.0%;	Pred. No. 0;		
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RESULT 2  
US-10-622-774-9  
; Sequence 9, Application US/10622774  
; Publication No. US20050022270A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Kentucky Research Foundation  
; APPLICANT: Hildebrand, David  
; APPLICANT: Hatanaka, Tomoko  
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSOXYGENASE GENE  
; FILE REFERENCE: 050229-0377  
; CURRENT APPLICATION NUMBER: US/10/622,774  
; PRIOR FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 60/396,406  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 1364  
; TYPE: DNA  
; ORGANISM: Veronia galamensis  
US-10-622-774-9

Query Match 61.9%; Score 870; DB 9; Length 1364;  
Best Local Similarity 86.1%; Pred. No. 7.5e-228;  
Matches 963; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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180 TAAAGAAAGCAATCCCTGCACATTCCTTCGCGCGCATCGCGCTCTGGTTCATCTGCTAGC 239  
209 TAAAGAAAGCAATCCCTCGCATTCCTTCGACGATCTGCCATCGTTTCATCGTCTAGC 268  
240 TAGTTCAAGATCTCATATACCTTCCTTTTATACAGGTCGCGCAACCTACATCTCTC 299  
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300 ACCTCCCTCCTCTAGTTTACTAGCATCGCGGTTTACTGTTTTCGCAATCTTGCA 359  
329 TCTTCTCCTCCTCTACCTTACTTAGCATGCGCTGTTTACTGTTTTCGCAATCTTGCA 388  
360 TCCTCCTCTGTTTATGGTCTCTCGCCATGAATCGCGCATCATGCTTTCAGTGAAGTACC 419  
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660 TCTTAACGAATGTTTTCAGGCAAGATGATAGATTTTACCAACCACTTTGATTCATTTGA 719

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Db 689 TCTTGACCAATATTTTCAGGCAAGAAATACAAAGGTTTGCACCACTTTGATCCGTTGA 748
QY 720 GCCCGATCTTACCGGAGCGTGACGGAATCCAGGTTCGGTTATCAGATCTTTGGTATCGTTG 779
Db 749 GCCCCATCTTCACTGAGCGTGACGAATCCAGGTTCGGTTATCAGATCTTTGGTATCGTTG 808
QY 780 CAGTGTTTACGAGCTCAAGTTCTTTGTGACAAACAAAGAGTTTGGTGGGTGATGCA 839
Db 809 CTGTGTTTACGGGCTTAAAGTTCTTTGTAGCGAAAAAAGGGTTCCGGTTGGGTAATCGCA 868
QY 840 TGTATCGAGTTCCAGTGATAGGTCGAATTCCTTCAATATCGTAATCACTTATCTGCACC 899
Db 869 TGTACGGAGCCCGAGTGGTGGGCTGAATGCCCTTCAATAATGATCACTTATCTCCACC 928
QY 900 ACACATCTGTCTGTCACCCCATTTAGCATTTCAACCGAATGGAATCGAATCAAGAGGACCT 959
Db 929 ACACCATCTGTCTGCGCTCATTAAGTTTCGACCGAATGGAATCGAATCAAGAGGACCT 988
QY 960 TGACCAATTCGACAGAGATTTTCGGTCTCTGTAATCCGTTTTCACGAGTTACACACA 1019
Db 989 TGACTACAATTCGATAGAGATTTTCGGTCTCTGTAATAGGGTGTTCATGACGTCATCACA 1048
QY 1020 CCCACGTGTGCACCAATTTGTTTCCCTACATTCACATTCATCATGCAAGGAGGCAAGCG 1079
Db 1049 CACACGTGTGCATCATTTTGTCCCGTACATTCACATTCATCATGCAAGGAGGCGAGCG 1108
QY 1080 AGGCCATCAAGCCAAATCTTGGGTGATTCAGAGGATGATCGACAGGACTCCATTTTCAAAG 1139
Db 1109 ACGCATAAAGCCGGTGTAGGGAGTATCGATGATGATGATGATGATGATGATGATGATGAT 1168
QY 1140 CAATGTGGAGAGGCGCAAGGAATGATTCATTCATGAGCAAGATGATGATGATGATGATGATGAT 1199
Db 1169 CAATGTGGAGAGGCGCAAGGAATGATTCATTCATGAGCAAGATGATGATGATGATGATGATGAT 1228
QY 1200 AAGGACATATTTGTTACCAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1237
Db 1229 AAGGTGATATTTGTTACCAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266

RESULT 3
US-10-912-534-131
; Sequence 131, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Stokesia laevis B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1134)
US-10-912-534-131

```

Query Match 49.6%; Score 697; DB 10; Length 1137;  
 Best Local Similarity 75.8%; Pred. No. 2.5e-180;

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Matches 862; Conservative 0; Mismatches 275; Indels 0; Gaps 0;
QY 92 ATGTCCGATTTCATATGATGATCAATGAAGATCATGATATGAGCAAGACGCCCCGATT 151
Db 1 ATGGCTTCTCTCTATGACGACAGAAATGAAGGACCATGATATGATGAAGAGACCAATTT 60
QY 152 GATCCGGCGCCATCTCGTTAAGTATGATCTAAAGAAAGCAATCCCTGCACATTCGTTCCGG 211
Db 61 GACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 212 CGATCCGCGCTCTGGTCACTCTGCTACGTAGTTCAGGATCTCATATCACTTCTCTTTTA 271
Db 121 AGATCTGCTGTTGGTCTCTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 272 TACAGGTGCGCAACACCTTACATCTCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 331
Db 181 TATCTGTGGCTAAACATTTATATTCACATCTTCCACCTTCCACTTGTCTCTCTCTCTCT 240
QY 332 CCGGTTTACTGGTTCGCAATCTTGCATCTCTCACTGGTTTATGGTCTCTCGCCATGAA 391
Db 241 CCAGTGTATTTGGTTCGCAATCTTGCATCTCTTACCTGGAATTTGGGTTCTTGGACATGA 300
QY 392 TCGGCGCATCATGCTCTTGTAGTGAGTACAGTGGATTTGATAAGCCGCTTGGATTCGTCCTC 451
Db 301 TCGGACATCATGCTCTTCTGAGTATCAATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 452 CATTCGGCTCTCTCAACCCCTTACTTTCTTGGAAATACAGCCATTCGAAAGCAACATGCA 511
Db 361 CATTCGCTCTTTCGATCTCATATTTCTTCTGGAAGTATTTCTCATAGAAAGCATCATGCT 420
QY 512 AACACAAATTCATCGAAGACGAGGAGTTTACATCTCTAGAACTCAGTCCCGCTCAGG 571
Db 421 AACACTAACTCTCTTGAAGAACGAGGAGTGTATTTTCAAGAACTCAATCTCAACTTGA 480
QY 572 ACTTACTCCACATACGAATTTCTTGCACACACGCTGCTGGTGAATCTCTCATCTTGGTCATC 631
Db 481 ACTTATTTCTATTTAGGTTCTTGCACACACTCTCAGGAAAGATTTCTTATTTCTTGTGAT 540
QY 632 ATGTTAACTTAGGATTTCTTTTATACCTCTTTAAAGCAATTTTTCAGGCAAGAGTACGAT 691
Db 541 ATGCTTACTCTTGGATTTCCCACTTTTATCTTTTGAATAAGCTCTCTGGAAGAGTATGAC 600
QY 692 AGATTTACCAACACTTTGATCCATTTGACCCGATCTTCCAGGCGGTGAGGGAATCCAG 751
Db 601 AGATTCACCTAACTTTTCGACCCACTTTCTCCAAATTTTTCACCTGAGAGAGAGAAATTC 660
QY 752 GTTGGCTTATCAGATCTTGGTATCGTTGAGGTTTTCAGGACTCAAGTTTCTTGTACAA 811
Db 661 GTTGTCTTTCTGATCTTGGAAATTTGGGCTGTGTTCTATGGACTTAAAGTTCTTGTTCAA 720
QY 812 ACAAAGGATTTGGTGGGTGATGTCATGATGGAGTTTCCAGTGTAGGTCTGAAATTC 871
Db 721 ACTAAGGATTTGGATGGGTTATGTCATGATGGATGTCAGTGTGACTTAACTCT 780
QY 872 TTCAATTCGTAATCACTTATCTGACCAACACATCTCTGCTGCTCAGCCCATTTACGATTC 931
Db 781 TTCAATTTGATTAATCTTATCTTATCATCTCATCTCTTCTTCTCTCCACTTATGATTTCT 840
QY 932 ACCGATGGAATCGGATCAAGGAGCTTGCACCAATTCGACAGATTTTCGCTCTCCG 991
Db 841 ACTGAGTGAATCGGATTAAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 992 AATCGGGTTTTCACGACGTTTACACACACCCAGTGTGTCACCATTTTGTTCCTTACATTT 1051
Db 901 AACAGAGTTTCCATGACGCTGACTCATCTCATGCTGCTTCTCATCACTTTTCCATATTT 960
QY 1052 CCACATTTATCATGCAAGAGGAGGCAACGAGGCGCATCAAGCCAAATCTTGGTGTATTCAGG 1111
Db 961 CCACATTTATCATGCTAAAGGAGGCTTCTGAGGCTTATTAAGCCAAATCTTGGAGCATATAG 1020
QY 1112 ATGATCGACAGGACTTCCATTTTTCAGCAATGTTGAGAGAGGCGCAAGAAATGCAATTTAC 1171
Db 1021 ATGATTTGATAGAACTCCATTTTTCAGGCTATGTTGGAGAGAGGCTTAAGGATGATCTAT 1080

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Matches		835;	Conservative	0;	Mismatches	229;	Indels	6;	Gaps	1;
QY	159	CGCATCTCTGTTAGTGTCTAAAGAAAGCAATCCCTGCACATTCCTTCGGCGATCCG	218							
Db	71	CACCTTTGACATTAAGTGTATTAAGAAAGCAATCCCTCCCATTCGTTCAAGCATCTG	130							
QY	219	CGCTCTGGTCACTCTGCTAGTGTTCAGATCTCATATATCATCTTCTCTTATACACGG	278							
Db	131	TCATACGTTTCGCTACTATGTGTGTTCATGATCTCATCGTCTCTCTACGCTCTCTTCTCC	190							
QY	279	TGCGCAACACCTACATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	338							
Db	191	TGCGCAACACATATATCT	250							
QY	339	ACTGTTTTCGCAATCTTTCGATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	398							
Db	251	ACTGTTTTCGCAATCTTTCGATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	310							
QY	399	ATCATGCTTTTGTAGTGTACGATGTGATTAACGCGGTTCGATTCGATTCGATTCGATTCG	458							
Db	311	ACCATGCTTTTGTAGTGTACGATGTGATTAACGCGGTTCGATTCGATTCGATTCGATTCG	370							
QY	459	CTCTCTCTCACT	518							
Db	371	CTCTCTCTCACT	430							
QY	519	ATTCACTCGAAACGAGGAAAGTTTACATTCCTAGAACTCAGTCCCAAGCTCAGGACTTACT	578							
Db	431	ATTCACTCGAAACGAGGAAAGTTTACATTCCTAGAACTCAGTCCCAAGCTCAGGACTTACT	490							
QY	579	CCACATACGAATTTCTTGTACACACGCTCTGTGATTCCTCATCTTGGTTCATCATCTTAA	638							
Db	491	CCA-----AAATCTCTAAACCAACCCACCTCGAAGGGTGTCTCTCTCTCTCTCTCTCTCT	544							
QY	639	CCTTAGGATTTCTCTTTATACCTCTTAAACGAAATGTTTCAGGCAAGAGTACGATAGATTA	698							
Db	545	CTCTAGGGTTTCTCTTTGTACCTTGTAACTTAATATCTCTGGAAGAAATACCAAGGTTTG	604							
QY	699	CCAACCACTTTTGATTCATTCATTCGAGCCGATCTTCAACGAGCGTGAGCGAATCCAGGTTGCGT	758							

RESULT 6  
US-10-772-227-33  
; Sequence 33, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbsky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Stokesia laevis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1131)  
US-10-772-227-33

Query Match		47.3%;	Score	665.6;	DB	8;	Length	1134;
Best Local Similarity		77.1%;	Pred. No.	1.1e-171;				
Matches		825;	Conservative	0;	Mismatches	239;	Indels	6;
Gaps		1;						
QY	159	CGCCATTCCTGTTAGTGTATCTAAAGAAAGCAATCCCTGCACATTCCTTCGGCGATCCG	218					
Db	71	CACCTTTACATTAAGTGTATATAAGAAAGCAATCCCTCCCATTCGTTCAAAAGGTCG	130					
QY	219	CGCTCTGGTCACTCTGCTAGTGTTCAGGATCTCATATACATTCCTCTCTTTTATACACGG	278					
Db	131	TCATAGGTCCTTACATCTATGTGTTCATGATCTCATCTCTCTCTCTCTCTCTCTCTCTCT	190					
QY	279	TGCGCAACACCTACATTCCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	338					
Db	191	TGCGCACTACATATATCT	250					
QY	339	ACTGTTTTCGCAATCTTTCGATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	398					
Db	251	ACTGTTTTCGCAATCTTTCGATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	310					
QY	399	ATCATGCTTTTGTAGTGTACGATGTGATTAACGCGGTTCGATTCGATTCGATTCGATTCG	458					
Db	311	ACCATGCTTTTGTAGTGTACGATGTGATTAACGCGGTTCGATTCGATTCGATTCGATTCG	370					
QY	459	CTCTCTCTCACT	518					
Db	371	CTCTCTCTCACT	430					
QY	519	ATTCACTCGAAACGAGGAAAGTTTACATTCCTAGAACTCAGTCCCAAGCTCAGGACTTACT	578					
Db	431	ATTCACTCGAAACGAGGAAAGTTTACATTCCTAGAACTCAGTCCCAAGCTCAGGACTTACT	490					
QY	579	CCACATACGAATTTCTTGTACACACGCTCTGTGATTCCTCATCTTGGTTCATCATCTTAA	638					
Db	491	CCA-----AAATCTCTAAACCAACCCACCTCGAAGGGTGTCTCTCTCTCTCTCTCTCTCT	544					
QY	639	CCTTAGGATTTCTCTTTATACCTCTTAAACGAAATGTTTCAGGCAAGAGTACGATAGATTA	698					
Db	545	CTCTAGGGTTTCTCTTTGTACCTTGTAACTTAATATCTCTGGAAGAAATACCAAGGTTTG	604					
QY	699	CCAACCACTTTTGATTCATTCATTCGAGCCGATCTTCAACGAGCGTGAGCGAATCCAGGTTGCGT	758					

Db 605 CCAACCACTTTGATCCATTTGATGCCATCTTACCGAGAGGAAAGGATTCAGGTCTTGG 664  
Qy 759 TATCAGATCTTGGTATCGTGCAGTGTGTTTACGAGCTCAAGTCTTCTGTACAAACAAAG 818  
Db 665 TATCAGATCTTGGTCTTCTAGCTGTAACTACGCAATCAAGCTTCTTGTGCTGCAAAAG 724  
Qy 819 GATTGGTGTGGGTGATGTCATGTATGAGGTTCAGTGTATAGGTCTGAATTCCTTCAATTA 878  
Db 725 GAGCTGTCTGGGTGACATGTCATCTATGGAGTTCAGTCTAGGTGTAAAGCGTGTCTTTCG 784  
Qy 879 TCGTAATCAGTATCTGACACACACATCTGTCTACCCCATTTACGATTCACCGGAAT 938  
Db 785 TTTTGTATCAGTATCTGACACACACATCTGTCTACCCCATTTACGATTCACCGGAAT 844  
Qy 939 GGAATCGATCAAGAGGAGCTTTCACACATCGACAGAGATTTTCGGTCTCTCTGAATCGGG 998  
Db 845 GGAATCGATCAGAGGAGCTTTCACACATCGATAGGATTTTGGGTCTCTAAATAGGG 904  
Qy 999 TTTTCCAGCTTACACACACACACAGTGTGACACATTTGTTCCCTTACATTCACATTT 1058  
Db 905 TTTTCCATGAGCTTACACACACATCTATGATTTGATTCATTTGATCTCTTACATTCACACT 964  
Qy 1059 ATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1118  
Db 965 ATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1024  
Qy 1119 ACAGGACTTCCATTTTCAAGCAATGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
Db 1025 ATAGGACTTCCATTTTCAAGCAATGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1084  
Qy 1179 AAGATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228  
Db 1085 CAGATGAAGATGACTGACACAAAGGGGTGTTACTGGTACCAATAAATGTAA 1134

## RESULT 7

US-10-912-534-33  
; Sequence 33, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeke, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Klook, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hreko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Deryck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Stokesia laevis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1131)  
US-10-912-534-33

Query Match 47.3%; Score 665.6; DB 10; Length 1134;  
Best Local Similarity 77.1%; Pred. No. 1.1e-171;  
Matches 825; Conservative 0; Mismatches 239; Indels 6; Gaps 1;

Qy 159 CGCCATTCGTGATGATCTTAAGAGAGCAATCCCTGACATGCTTCCGGCGATCG 218

Db 71 CACCTTTTCATTAAGTATATAAAGAAAGCAATCCCTCCCATTTGCTTCAAAAGGTCTG 130  
Qy 219 CCGTCTCGTCACTCTGCTAGTTCAGGATCTCATTAACAATCTCTCTTTTATACACGG 278  
Db 131 TCATAAGGTCTTCATATATGTTTTCATGATCTCATCGTCTCCTAGGTCTTCTTCTTCC 190  
Qy 279 TCGCAACACTTACATTTCTCCTCCTCTCTAGTTTATCTTATAGCATGGCGGTTT 338  
Db 191 TCGCAACTATATATTAATTAATTTCTTCTCTCTCTCTTATCATAGCTTGGCCAGTTT 250  
Qy 339 ACTGGTTTTCGCAATCTTTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 398  
Db 251 ACTGGTTTTCGCAAGCAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 310  
Qy 399 ATCATGCTTTTATGAGTACAGTGGATGATTAACGCGGTGGATTCGTCTCTCAATTCGG 458  
Db 311 ACCATGCTTTTATGATTAACAGTGGATGATGACACAGTGGGTTCATCTCTCACTCTG 370  
Qy 459 CTCTCTCTCAACCAAGAGGATTTTACATTTCTAGAACTCAGTCCCTCAGTCTCAGGACTTACT 518  
Db 371 CTCTCTCTCAACCAAGAGGATTTTACATTTCTAGAACTCAGTCCCTCAGTCTCAGGACTTACT 430  
Qy 519 ATTCAGTCTGAAAGAGGATTTTACATTTCTAGAACTCAGTCCCTCAGTCTCAGGACTTACT 578  
Db 431 ATTCAGTCTGAAAGAGGATTTTACATTTCTAGAACTCAGTCCCTCAGTCTCAGGACTTACT 490  
Qy 579 CCAATATGAAATTTCTTGAACACGCTGGTTCGAACTCTCTCTCTCTCTCTCTCTCTCTCTCT 638  
Db 491 CCA-----AAATCTTAAACCAACCACTGGAAGGGTTCCTCTCTCTCTCTCTCTCTCTCTCT 544  
Qy 639 CTTTAGATTTCTCTTATCTCTTAAAGATTTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 698  
Db 545 CTCTAGGGTTTCTCTTGTACCTGTTAACTAATATCTCTGGAAGAAATACCAAAAGTTTG 604  
Qy 699 CCAACCACTTTGATCTGAGCGGATCTTACCGAGCGTACGCGGATTCAGGTTGCGT 758  
Db 605 CCAACCACTTTGATCTGAGCGGATCTTACCGAGCGTACGCGGATTCAGGTTGCGT 664  
Qy 759 TATCAGATCTTGGTATCGTTCAGTGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 818  
Db 665 TATCAGATCTTGGTATCGTTCAGTGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 724  
Qy 819 GATTGGTGGTGTATGTCATGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 878  
Db 725 GAGCTGTCTGGGTGACATGTCATCTAGGAGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGG 784  
Qy 879 TCGTAATCAGTATCTGACACACACATCTGTCTGTCACCCCATTTACGATTCACCGGAAT 938  
Db 785 TTTTGTATCAGTATCTGACACACACATCTGTCTGTCACCCCATTTACGATTCACCGGAAT 844  
Qy 939 GGAATCGATCAAGAGGAGCTTTCACCAATCGACAGAGATTCGGTCTCTCTGAATCGGG 998  
Db 845 GGAATCGATCAGAGGAGCTTTCACCAATCGATAGGATTTTGGGTTCCTAAATAGGG 904  
Qy 999 TTTTCCAGGAGGATTCACACACACAGTGTGACACATTTGTTCCCTTACATTCACATTT 1058  
Db 905 TTTTCCATGAGCTTACACACACATCTATGATTTGATTCATTTGATCTCTTACATTCACACT 964  
Qy 1059 ATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1118  
Db 965 ATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1024  
Qy 1119 ACAGGACTTCCATTTTCAAGCAATGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
Db 1025 ATAGGACTTCCATTTTCAAGCAATGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1084  
Qy 1179 AAGATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228  
Db 1085 CAGATGAAGATGACTGACACAAAGGGGTGTTACTGGTACCAATAAATGTAA 1134

## RESULT 8

US-10-772-227-6

```

; Sequence 6, Application US/10772227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Hresko, Michelle Coutu
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Crepis biennis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1122)
; US-10-772-227-6

Query Match 46.8%; Score 657.8; DB 8; Length 1125;
Best Local Similarity 75.6%; Pred. No. 1.5e-169;
Matches 847; Conservative 0; Mismatches 262; Indels 12; Gaps 2;

Qy 108 ATGATCGAATGAAGATCATGATAGGACGACCGGATTCGATCGGCGCATCTCT 167
Db 17 ATGCTCGAATCGAAGAAATCGTATGGAACGTTCTCGGTTGATCCAGTACCCCTCT 76

Qy 168 CGTTAGTATGATTAAGAAAGCAATCCCTGCACTTCTCGGCGATCCGCGTCTGGT 227
Db 77 CGCTAAGTATGATTAAGAAAGCAATCCCTCGGATTCGATCGGCGATCTCTGTCATCG 136

Qy 228 CATCTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 287
Db 137 CATCTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196

Qy 288 CCTACATCTCTACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 347
Db 197 AATATATTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256

Qy 348 GCAATCTTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 407
Db 257 GTCAAGTATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 316

Qy 408 TTAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
Db 317 TTAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376

Qy 468 CCCCTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 527
Db 377 CCCCTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 436

Qy 528 AAAACGAGGAGTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 587
Db 437 ATAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490

Qy 588 AATTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 647
Db 491 AATTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 550

Qy 648 TTCTCTTATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 707
Db 551 TTCTCTTATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 610

Qy 708 TTGATCCATTTGAGCCCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 767

```

17 ATGTCGACATCGAATAAATCGGTCATGGAACGTGCTCGGTTGATCCAGTACCCCTTCT 76  
168 CGTTAAGTGATCTAAGAAAGCAATCCCTGACATGTTGCTTCGGCGATCCGCGGTCGTGGT 227  
77 CGCTAAGTGATTTAAGCAAGCAATCCCTCCCAATGCTTCGAGCGATCTGTCATCCCGTT 136  
228 CATCTGCTAGCTAGTTCAGGATCTCATATACACCTTCCTTTTATACAGCGTCGCGCAACA 287  
137 CATCTTACTATATGTTACGATCTCATATATGCGCTACATCTTCTTACTTCCTTGGCGATA 196  
288 CCTACATTCCTCACCTCCCTCCTCTCTAGTTTACTTAGCATGGCGGTTTACTGGTTT 347  
197 AATATATTCGAGTTCCTCTGCTCTCTAGCTACTTAGCTTGGCCCTTTACTGGTTCT 256  
348 GCCAATCTTGCATCCTACTGTTTATGGGTCCTCGGCCATGAAATCGCGCATCATGCGT 407  
257 GTCAGCTAGCATCCTCACTGGTTTATGGATCTCTCGGTCATGAATCGCGTCACCATGCGT 316  
408 TTAGTGAGTACAGTGGATGATTAACGCGGTTGGATTGCTCTCCATTCGGCTCTCCCTCA 467  
317 TTAGCGAGTACCAATGGGTTGACGACACTGTGGGCTTCATGGTCCACTCATTTCTCCCTCA 376  
468 CCCCTTACTTTCTTGGAAATACAGCCATCGAAAGCACCATGCAAAACACAAATTCACCTCG 527  
377 CCCCGTATTTCTGTGGAAATACAGTACCGGATCACCATGCCAACAACAGTTCATCG 436  
528 AAAACGAGGAATTTACATTCCTTAGAATCTAGTCCAGCTCAGGACTTACTCCACATACG 587  
437 ATAACGATGAAGTTTACATTCGGAAGCAAGTCCAAACTCGCGCTT-----ACCTATA 490  
588 AATTTCTTGACAAACGCTGCTGATCCTCATCTTGGTCATCATGTTTAACTTAGGT 647  
491 AACTTTCTTAACAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
648 TTCCCTTTATACCTTTAAGCAATGTTTCAAGCAAGTACGATAGATTTACCAACCACT 707  
551 TTCCCTTTATACCTTTGACAAATATTTCCGGCAAGAGTACGACAGGTTTGGCAACCACT 610  
708 TTGATCCATTTGAGCCGATCTTTCACCGAGCGGTGAGCGAATCCAGGTTCGGTTTATCAGATC 767  
611 TCGACCCCATGAGTCCAAATTTTCAAGGAAGTGTGAGCGGTTTCAGGTCCTTTCGGATC 670  
768 TTGGTATCGTTCAGTGTGTTTACGAGTCAAGTTCCTGTTGTACAAACAAAGATTTGGTT 827  
671 TTGGGCTTCTCTGCTGTTTATGGAATTTAAAGTTGCTGTAGCAAGAAAGAGCTGCGT 730  
828 GGGTGATGTGATGATGAGTTTCCAGTGATAGGTCGTAATTCCTTCAATTCGTAATCA 887  
731 GGGTGGGTGATGATGAGTTTCCGATGCTAGGCGTATTTAACCTTTTCGATATCATCA 790  
888 CTTATCTGCACACACATCTGTCGTCAACCCATTTACGATTTCAACCGAATGGAACTGGA 947  
791 CGTACTTGACACACACCCATCAGTCGTCTCTCATTTATGACTCAACTGAATGGAACTGGA 850  
948 TCAAGAGGCGTGTGACCAACATCGACAGATTTCCGTCCTCGATCGGTTTTCACG 1007  
851 TCAGAGGGGCGTGTGAGCAATCGATAGGAGCTTTGGGTTTCATGATGATGTTTCCATG 910  
1008 AGTTTACACACACACCGAGTGTGACCACTTTGTTTCCCTTACATTCACATTTATCATGAA 1067  
911 ATGTTTACACACACTCAGTCATGATCATATGTTTTCATACATTTCCACACTATCATGGA 970  
1068 AGGAGGCAAGCGAGCCATCAAGCCAACTTCCTGGGTGATTTACAGGATGATCGACAGACTC 1127  
971 AAGAGCAAGGGATGCAATCAATACTATAGGCGACTATTATATGATGATGATGAGACTC 1030  
1128 CATTTTTCAGCAATGTGAGAGAGGCCAAGGATGCAATTTTACATCGAGCAAGATGAG 1187  
1031 CAATTTTGAAGCACTGTGAGAGAGGCCAAGGATGCAATTTTACATCGAGC-----CTG 1084  
1188 ACAGCAAGCACAAGAGGACATATTTGGTACCATATAAATGTAA 1228  
947 GTGGGCTTTCATCATCCCATTTCTCTCTCAGCCCGTATTTCTCTTGGAAATACAGTAC 427  
947 CGAAAGCCATGCAATTCCTCTCGAATAACAAATTCCTCGAATAACAGGAGTTTACATTCCTAGAACT 556

RESULT 10

US-09-981-124-3  
; Sequence 3, Application US/09981124  
; Patent No. US20020166144A1

GENERAL INFORMATION:

; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: PATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
; TITLE OF INVENTION: PATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
; FILE REFERENCE: 26-98A

; CURRENT APPLICATION NUMBER: US/09/981.124

; CURRENT FILING DATE: 2001-10-17

; PRIOR APPLICATION NUMBER: US 09/059769

; PRIOR FILING DATE: 1998-04-14

; PRIOR APPLICATION NUMBER: US 60/043706

; PRIOR FILING DATE: 1997-04-16

; PRIOR APPLICATION NUMBER: AU P06223

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: AU P06226

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: US 60/050403

; PRIOR FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1309

; TYPE: DNA

; ORGANISM: Crepis sp.

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (937)..(937)

; OTHER INFORMATION: N is any nucleotide residue

; NAME/KEY: CDS

; LOCATION: (26)..(1147)

; OTHER INFORMATION:

; NAME/KEY: misc feature

; LOCATION: (901)..(901)

; OTHER INFORMATION: N is any nucleotide residue

US-09-981-124-3

Query Match 46.8%; Score 657.6; DB 3; Length 1309;

Best Local Similarity 76.4%; Pred. No. 1.8e-169;

Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTTGATCCGCGCATTTCTCGTTAAGTGATCTAAAGAAAGCAATCCCT 196

DB 68 GAACGTGTCTCAGTTGATCCAGTAAACCTTCTCAGTGAGTATTGACGAGCAATCCCT 127

QY 197 GCACATTCTCTTCGCGCGATCCGCGCTGTGTCATCTCTGCTACGTAGTTTCAGGATCTCAT 256

DB 128 CCACATTCTCTTCGAGCGATCTGTATCGTTTCATCTTATAGTTGTTTCAGGATCTCATA 187

QY 257 ATACCTTCTCTTTTATACACGGTCGCGCAACACCTACATTTCTCACCCTCCCTCTCTCTA 316

DB 188 ATTGCTACATCTTCTACTTCTCTTCCCAACACATATATCCCTAATCTCCCTCATCTCTA 247

QY 317 GTTTACTTTAGCATGCGCGTTTACTGGTTTTCGCAATCTTGCATCTCTCAGTGGTTTATGG 376

DB 248 GCCTACTTGTAGCTTGGCCGCTTTACTGGTTCTGTCAAGTAGGTCCTCAGTGGTTTATGG 307

QY 377 GTCTCTCGGCCATGAAATGCGGCCATCATGCTTTTACTAGTAGTACCACTGGAATGATTAACGCC 436

DB 308 ATCTCTCGGCCATGAAATGCGGCCATCATGCTTATGCAACATACACATGGGTTGACGACACT 367

QY 437 GTTGAATTCGCTCTCCATTCGCTCTCTCTCACCCTTACTTTTCTTGGAAATACAGCCAT 496

DB 368 GTGGGCTTTCATCATCCCATTTCTCTCTCAGCCCGTATTTCTCTTGGAAATACAGTAC 427

QY 497 CGAAAGCCATGCAACAAATTCCTCGAATAACAGGAGTTTACATTCCTTAGAACT 556

Db 428 CGGAATCACCATTCCAACAAGTTCGATTGATAAGCATGAAGTTACATTCGAAAAGC 487  
Qy 557 CAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACGCGCTGTGGAATC 616  
Db 488 AAGTCNAACCAAGGT-----ATCTATAAATCTTTAAACAACCCACCTGTGCACTG 541  
Qy 617 CTCACTCTGTGTCATATGTTAACTTAGGATTTCTTTATACCTTTTAAACGAATGTTCA 676  
Db 542 TTGGTTTGGTTATCATGTTTCACTTAGGATTTCTTTATACCTTTGACAAATATTTCC 601  
Qy 677 GGAAGAAGTACATAGATTACCAACCACTTTGATCCATTGAGCCGGATCTTACCGAG 736  
Db 602 GGAAGAATAACATAGTTTGGCAACCACTTCGACCCCAATGATGCCAATTTTCAAGAA 661  
Qy 737 CGTGAGCGAATCAGGTTGGTTATCAGATCTTGGTATCGTTCAGTGTGTTTACGCACTC 796  
Db 662 CGTGAGCGGTTTCAGTCTTCTTTCGATCTTGGTCTTCTGCTGTGTTTATGAAAT 721  
Qy 797 AAGTTTCTTGTACAAACAAAGGATTTGGTTGGGTGATGTGCAATGATGAGTTCAGTG 856  
Db 722 AAGTTTCTGTAGCAAAATAAGGAGCTGCTTGGGTGGGTGCAATGATGAGTTCGGTG 781  
Qy 857 ATAGGTCTGAATTCCTTATATTCGTAATCACTTATCTGACCAACACACATCTGTCTCA 916  
Db 782 CTAGGCGTATTTACCTTTTTCGATGTGATCACTGTTCTTACCAACACCACTCATGCTCG 841  
Qy 917 CCCCATTAGATTCAACCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGA 976  
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Qy 977 GATTTCGGTCTCTGAAATCGGTTTTTCCACAGGTTTACACACACCACTGTTGCAACCAT 1036  
Db 902 GACTTTGGGTTCTGATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGAT 961  
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Db 962 TTGTTTTCATACATTCACACTATCATGCAAGGAGGCAAGGCAAGGCAAGGCAAGGCA 1021  
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Db 1022 TTGGGCGACTTTTATATGATCGATGAGTCCAAATTTTAAAGCAATGAGGAGGCG 1081  
Qy 1157 AAGGAATGCAATTTACATTCGAGCAAGATGCAAGCAAGCAAGCAAGCAAGCAATTTGGTAC 1216  
Db 1082 AGGAATGCAATGATGATGAGTCCAAATTTTAAAGCAATGAGGAGGCG 1135  
Qy 1217 CATAAATGTAATC 1230  
Db 1136 CATAAATGTAATC 1149

## RESULT 11

US-10-772-227-12  
; Sequence 12, Application US/1077227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbsky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloeck, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLeod, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772, 227  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Crepis biennis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1140)  
; US-10-772-227-12  
  
Query Match 45.9%; Score 646; DB 8; Length 1143;  
Best Local Similarity 73.8%; Pred. No. 2.6e-166;  
Matches 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2;  
  
Qy 75 TGGAGAAGGTAGCAGAATGTGGATTTCATATGATGATCGAATGAAGAAGTATCATGATG 134  
Db 2 TGGGTGAGGTGGAAGATGCGGGTCTTCTTCCAAAGAAATCGAAACCGACACCA 61  
Qy 135 ACGAAGAGCCCGGATGATCGCGGCCATCTCGTTAAGTGTCTAAGAAAGCAATCC 194  
Db 62 CAAAGCGTGTGCGGTGCGAGAAACCGCCCTTTCTCGGTGGAGATCTGAAGAAAGCAATCC 121  
Qy 195 CTGCACATTTGCTTCGCGCATCGCGTCTGGTTCATCTGCTACGTAGTTCAGGATCTCA 254  
Db 122 CCCCCATTTGCTTCAGCGATCTGTAATCGTTCATCTTACTATGTAGTTCAGATCTCA 181  
Qy 255 TTATCACCTTCTCTTTTATACAGGTGCGCAACACCTTACATTCCTCACCTCCCTCCTC 314  
Db 182 TTATTGCTTACATCTTCTTCTTCTGCGATAAATATATTCGATTTCTCCCTGCTCCTC 241  
Qy 315 TAGTTTACTTAGATGCGCGGTTTACTGTTTGGCAATCTTGCAATCTTGCAATCTGCTGTTAT 374  
Db 242 TAGCTTACTTAGTGTGCGCCCTTTTACTGTTCTGTCAAGTAGCATCTCCTCCTGTTAT 301  
Qy 375 GGGTCTCGCGCATGAATCGGCCATCATGCGCTTTAGTGTAGTACAGTGGATTGATAACG 434  
Db 302 GGATCTCTCGGTCAATGAATGCGGTCACTGCTTTAGCGAGACCAATGGGTGAGACGA 361  
Qy 435 CGGTGGATTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 494  
Db 362 CTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 421  
Qy 495 ATCGAAGCAACATGCAAAACACAAATTTACTCGAAGAGGAGGATTTTACATTTCTTAGAA 554  
Db 422 ACCGAATCACCATGCGCAACACAAATTTCAATGATGAAGTTCATATTTCCGAAA 481  
Qy 555 CTCAGTCCAGCTCAGGACTTCTCCACATACGAATTTCTTGACACACGCTTGTGCGAA 614  
Db 482 GCAAGTCCAACTCGCGCTT-----ACCTATAAATCTTCTTAAACCCGCTGGTCCGAC 535  
Qy 615 TCCTCATCTTGGTTCATCATGTTAACTTAGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 674  
Db 536 TGTAGTTATGTTATCATGTTTCACTTAGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 595  
Qy 675 CAGGCAAGAAGTACGATAGATTTCACCACTTTGATCOATTGAGCCGATCTTCAACG 734  
Db 596 CCGGCAAGAAGTACGACAGGTTTGCACCACTTCGACCCCATGAGTCCAATTTTCAAGG 655  
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Db 716 TTAAGTTCTGTAGCAAGAAAGAGCTGCGTGGGTGGGTGATGTATGAGTTCGGA 775  
Qy 855 TGATAGTCTGAATTCCTTTTCTTATTCGTAATCATTTATCTGACACCAACATCTCTCGT 914  
Db 776 TGCTAGGCGTATTTACCTTTTTCGATATCATCAGTACTTGCACCAACACCCATCAGTCT 835  
Qy 915 CACCCCATTTACGATTCACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 974  
Db 836 CTCCTCATTTATGACTCACTCACTGAATGGAATGGAATGGAATGGAATGGAATGGAATG 895



QY 975 GAGATTTCGGTCTCCTGAATCGGGTTTTCCAGGAGTTACACACACCCACGTTGTCACC 1034  
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DB 1130 ATCATAAATTGTGA 1143  
RESULT 12  
US-10-912-534-12  
; Sequence 12, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Deryck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; TITLE OF INVENTION: PLANTS MADE THEREFROM  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Crepis biennis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1140)  
US-10-912-534-12  
Query Match 45.9%; Score 646; DB 10; Length 1143;  
Best Local Similarity 73.8%; Pred No. 2,6e-166;  
Matches 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2;  
QY 75 TGGGAGAAGGTAGCAGAATGTCGGATTTCATATGATGATCGAATCGAATGAAGATCATGATAGG 134  
DB 2 TGGGTGCGAGTGGAGAAATGCCGTTCTCTTCTTCCAAAGAAATCGGAACCGACACCA 61  
QY 135 ACGAAGGAGCCCGGATTTGATCGGGGCCATTTCTGTTAAGTATCTTAAGAAAGCAATCC 194  
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QY 195 CTGCAATTTCTCGGGCATCGCGCTGTGTCCTGTCCTGTCACGTAGTTTCAAGGATCTCA 254  
DB 122 CTCGCCATTTCTCAGCGCATCTGAATCCGTTTCATCTTACTATGTAGTTTCAAGATCTCA 181  
QY 255 TTATCACCTTCTTTTATACAGGTCGCAACACCTTACATTCCTCACCTCCCTCCCTCC 314  
DB 182 TTATTGCTTACATCTTCTACTTCTTCTGCGGATAAATATATTCGGATTTCTCCCTGCTC 241  
QY 315 TAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCAATCTTGGCATCTTCACTGTTTAT 374

DB 242 TAGCTACTTAGCTTGGCCCTTTACTGGTTCTGCTCAAGCTAGCATCTCTCACTGGTTAT 301  
QY 375 GGGTCTCGGCATGAATGCGGCCATCATGCTTTTAGTGAATCAAGTGGATTTGATAAG 434  
DB 302 GGATCTCTCGGTCAATGAATGCGGTCAACATGCTTTTAGCGAGCAATATGGGTGACGACA 361  
QY 435 CCGTTGGAATTCGTCTCATTTCGGCTCTCTCACCCCTTACTTTTCTTGGAAATACAGCC 494  
DB 362 CTGTGGGCTTCATGGTCCACTCATTTCTCTCTCACCCGATTTCTCTGTTGGAATATACATC 421  
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QY 555 CTCAGTCCCAGCTCAGGACTTACTCCACATACGAATTTCTTGAACAACAGCGCTGGTGA 614  
DB 482 GCAAGTCCAAACTCGCGCTT-----ACCTATAAATCTTTAAACAACCGCTGCTCGAC 535  
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QY 675 CAGCAAGAAGTACGATAGATTTTACCAACCACTTTTGATCCATTGAGCCCGATCTTCAACG 734  
DB 596 CCGCAAGAGTACGACAGGTTTGGCAACCACTTCGACCCCATGAGTCCAATTTTCAAG 655  
QY 735 AGCGTAGCGAATCAGGTTGCGTTATCAGATCTTGGTATCGTTGCGAGTGTTTTACGAC 794  
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DB 776 TGCTAGGCGTATTTACCTTTTTCGATATCATCATGCTACTTGCACCAACCCATCATGCT 835  
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QY 975 GAGATTTCGGTCTCCTGAATCGGGTTTTCCAGCGTTTACACACACCCACCGTTGTCACC 1034  
DB 896 GGGACTTTGGGTTCAATGAATAGTGTGTTTCCATGATGTTTACACACACTCACGTCATG 955  
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DB 956 ATATGTTTTCATACATTTCCACATTCATCATGCGAAGAGCGCAAGGATGCAATCAATCA 1015  
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QY 1155 CCAAGGAATGCAATTTACATCGAGCAAGATGCGAGCAGCAAGCAAAAGGACATATTGGT 1214  
DB 1076 CCAAGGAATGCAATGTACATCGAGC-----CTGATAGCAAGCGCAAGGTTGTTATTGGT 1129  
QY 1215 ACCATAAAATGTAA 1228  
DB 1130 ATCATAAATTGTGA 1143  
RESULT 13  
US-10-622-774-10  
; Sequence 10, Application US/10622774  
; Publication No. US20050022270A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Kentucky Research Foundation  
; APPLICANT: Hildebrand, David  
; APPLICANT: Hatanaka, Tomoko  
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPOSYGENASE GENE



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; FILE REFERENCE: 050229-0377
; CURRENT APPLICATION NUMBER: US/10/622,774
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/396,406
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Crepis palaestina
US-10-622-774-10

Query Match      45.5%; Score 640.4; DB 9; Length 1344;
Best Local Similarity 75.5%; Pred. No. 9.9e-165;
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCCGATTCGATCCGGCGCCATCTCGTTAAGTGATCTAAGAAAGCAATCCCT 196
DB 75 GAACGCTGCTCAGTTGATCCAGTAACCTTCTCACTGAGTGAATGAAGCAAGCAATCCCT 134

QY 197 GCACATTGCTCCGGCGATCCGGCGTCTGCTCATCTGCTAGCTAGTTCAGGATCTCAT 256
DB 135 CCCATGCTTCCAGAGATCTGTAATCCGCTCACTTACTATATGTTGTTCAAGATCTCAT 194

QY 257 ATCACCTTCCTTTTATACAGGTCGCGCAACACCTACATTCCTCACCTCCCTCTCTCTA 316
DB 195 ATTGCTACATCTTCTACTTCTTCCGCAACACATATATCCCTACTCTTCTACTAGTCTA 254

QY 317 GTTTACTAGCATGGCGGTTTACTGGTTTGGCAATCTTGCACTCTCATCTGTTTATGG 376
DB 255 GCGTACTAGCTTGGCCGTTTACTGGTTTCTGTCAAGCTAGCGTCTCTCACTGGCTTATGG 314

QY 377 GTCTCGGCCCAATGCGGCCATCATGCTTTAGTGAGTACCAGTGAATGTATACGCG 436
DB 315 ATCTCGGCCCAAGTGTGTCACCATGCTTTAGCAACTACACATGGTTTACGACACT 374

QY 437 GTTGAATTCGTCTCCATTCGGCTCTCTCCACCCCTTACTTTCTTGGAAATACAGCCAT 496
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QY 497 CGAAGCACATGCAAAACAAATTCATCGAAACAGAGAGTGTATTCATCTTAGAAT 556
DB 435 CGGAATCACCATTCCAACACAAAGTTCGATGATAACGATGAAGTTTACATTCGAAAGC 494

QY 557 CAGTCCAGCTCAGGACTTACTCCATACAGATTTCTTGACAAACGCGCTGTCGAATC 616
DB 495 AAGTCCAAACTCGCGCT-----ATCTATAAACTTCTTAACAAACCCACTGTCGCGTG 548

QY 617 CTCATCTTGTGTCATCATGTTAACTTTAGGATTTCTTTTATACCTCTTAACGAATGTTCA 676
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DB 609 GCGAAGAAATACGACAGGTTTGCAACCACTTCCGACCCCATGAGTCCAATTTTCAAGAA 668

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QY 917 CCCATTACGATTCACCGGAATGGAATCGAATCAAGAGGACCTTGACCAACATCGACAGA 976
DB 849 CCTCATTATGATTCAGTGAATCGAATCGGATCAGAGGGGCGCTTGTGAGCAATCGATAG 908
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QY 977 GATTTCCGTCCTCGAATCGGGTTTTCCACGACGTTTACACACCCACCGTGTGTGACCAT 1036
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QY 1037 TTGTTTCCCTACATTCACATTCATTCATGCAAGGAGGCAAGCGAGGCCATCAAGCAATC 1096
DB 969 TTGTTTTCATACATTCACACTATCATGCAAGGAGGCAAGGAGGATGCAATCAAGCCATC 1028

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QY 1157 AAGGAATGCAATTCATCGAGCAAGATCGACAGCAACGACCAAGGAGACATATGCTATC 1216
DB 1089 AGGGAGTGTGATGATCATCGAGC-----CTGATAGCAAGCTCAAAGGTGTTTATTGGTAT 1142

QY 1217 CATAAATGTAATC 1230
DB 1143 CATAAATGTGATC 1156

RESULT 14
US-09-981-124-1
; Sequence 1, Application US/09981124
; Patent No. US20020166144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Marit
; APPLICANT: Stymme, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MODI
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981,124
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1358
; TYPE: DNA
; ORGANISM: Crepis palaestina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1151)
; OTHER INFORMATION:
US-09-981-124-1

Query Match      45.5%; Score 640.4; DB 3; Length 1358;
Best Local Similarity 75.5%; Pred. No. 1e-164;
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCCGATTCGATCCGGCGCCATTCCTCGTTAAGTGATCTAAGAAAGCAATCCCT 196
DB 75 GAACGCTGCTCAGTTGATCCAGTAACCTTCTCACTGAGTGAATGAAGCAAGCAATCCCT 134

QY 197 GCACATTGCTCCGGCGATCCCGGCTGCTGCTCATCTGCTAGTGTAGTTCAGGATCTCAT 256
DB 135 CCCATGCTTCCAGAGATCTGTAATCCGCTCACTTACTATATGTTGTTCAAGATCTCAT 194

QY 257 ATCACCTTCCTTTTATACAGGTCGCGCAACACCTACATTCCTCACCTCCCTCTCTCTA 316
DB 195 ATTGCTACATCTTCTACTTCTTCCGCAACACATATATCCCTACTCTTCTACTAGTCTA 254
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QY 317 GTTTACTTAGCATGGCCGGTTTACTGGTTTGGCAATCTTGCAATCCCTCACTGGTTTATGG 376
Db 255 GCCTACTTAGCTTGGCCGGTTTACTGGTTTGTCAAGCTAGCGTCTCACTGGCTTATGG 314
QY 377 GTCCTCGGCCCATGAATGGGCCCATCATGCCCTTGTAGTGAGTACCAAGTGAATGAACGCC 436
Db 315 ATCTCTGGCCAGAAATGGTGCACATGCCCTTTAGCACTACACATGGTTTGACGACACT 374
QY 437 GTTGGATTCGTCCTCCATTCGGCTCTCTCTACCCCTTACTTTTCTTGGAAATACAGGCAT 496
Db 375 GTGGCTTCATCTCCACTCATCTCTCTCTACCCCGTATTTCTCTTGGAAATTCAGTCAC 434
QY 497 CGAAGACCAATGCAACACACAAATTCACGAAACGAGGAGTGTACATTCCTAGACT 556
Db 435 CGGAATCACCAATTCACACACAAGTTCGATTCGAATGAAGTGTACATTCGGAAGC 494
QY 557 CAGTCCCAAGCTCAGGACTTACTCCACATACGAATTTCTTGCAACACGCGCTGGTCGAATC 616
Db 495 AAGTCCAAACTCGCGCT-----ATCTATAAATCTTAAACACCCACCTGGTCGGCTG 548
QY 617 CTCATCTTGGTCATCATGTTAACTTTAGGATTTCTTTATACCTCTTAAACGAATGTTTCA 676
Db 549 TTGGTTTTGATTCATGTTTCACTGTTTCCCTTAGGATTTCTTTATACCTCTTGACAAATATTCC 608
QY 677 GGCAAGAGTAGGATAGATTTACCAACCACTTGTATCCATTTGAGCCCGATCTTCACCGAG 736
Db 609 GGCAGAAATACGACAGGTTTGGCAACCACTTCGACCCCATGAGTCCAAATTTCAAGAA 668
QY 737 CGTGAGCAATCCAGGTTGCGTTATTCAGATCTTGTGATCGTTGCAAGTGTATTCAGGACTC 796
Db 669 CGTGAGCGGTTTCAAGTCTCTCTTCGATCTTGGTCTCTTCCGCTGTTTATGGAAT 728
QY 797 AAGTTTCTTGACAAACAAAGGATTTGGTTGGGTGATGTGCATGATGAGGATTCAGT 856
Db 729 AAAGTTGCTGTAGCAATAAAGGAGCTGCTTGGGTAGCGTGCATGTATGAGGATTCGGTA 788
QY 857 ATAGTCTGAATCTCTTCAATTCGTATATCACTTATCTGACCAACACATCTGTCGTCA 916
Db 789 TTAGCGGTATTTACCTTTTTCATGTGATCACCTTTCTTGCACCAACACCCATCAGTCGTCG 848
QY 917 CCCATACGATTCACCGAATGGAATCGGATCAAGGAGGCTTGACCAACATCGACAGA 976
Db 849 CCTCATATGATTCATCTGAATGGAATCGGATCGAGGGGCTTGTGAGCAATCGATAGG 908
QY 977 GATTTGGGTCTCTGAAATCGGTTTTTCCACGAGTTTACACACACCCAGCTGTGACCAAT 1036
Db 909 GACTTTGGATTCCTGAAATAGTGTTTTCCATGATGTTTACACACACTCATGTATGATCAT 968
QY 1037 TTGTTTCCCTACATTCGACATATTCATGCAAGGAGGCAAGGAGGCCATCAAGCCAATC 1096
Db 969 TTGTTTTCATACATTCACACTATTCATGCAAGGAGGCAAGGAGTGCATCAAGCCAATC 1028
QY 1097 TTGGGTGATTCAGGATGATCGACAGGACTCCATTTTCAAGCAATGTGGAGAGGCCC 1156
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QY 1157 AAGGAATGCATTTATCATCGACAGATGACAGACGACAAAGGACATATTTGGTAC 1216
Db 1089 AGGGAGTCATGTACATCGAGC-----CTGATACGAAGCTCAAAGGTGTTTATTTGGTAT 1142
QY 1217 CATAAATGTAATC 1230
Db 1143 CATAAATGTTGATC 1156
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## RESULT 15

US-10-772-227-32

; Sequence 32, Application US/1077227

; Publication No. US20040168213A1

; GENERAL INFORMATION:

; APPLICANT: Verbsky, Michelle L.

; APPLICANT: Baublite, Catherine

; APPLICANT: Williams, Deryck J.

```
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaIRD, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1122)
US-10-772-227-32
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Query Match 45 43; Score 638.6; DB 8; Length 1125;

Best Local Similarity 74.5%; Pred. No. 2.8e-164; Indels 12; Gaps 2;

Matches 835; Conservative 0; Mismatches 274;

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QY 108 ATGATCGAATGAAAGATCATGATATGACGAACGAGCCCGATTTGATCCGGCGCATTTCT 167
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QY 168 GGTAAAGTATCTAAAGAAAGCAATCCCTGCACATTTGCTCCGGGATCCGCGCTCTGGT 227
Db 77 CTCTAAGTATTTGAAGCAAGCAATCCCTCCCAATGCTTCCAGCGATCTGTATCCGTT 136
QY 228 CATCTCTAGTATGATTCAGGATCTCATTTATACCTTCTCTTTTATACAGGTTCGCAACA 287
Db 137 CATCTTACTATGTAGTTCACGATCTCATTTATGCTCATCTTCTTCTTCTTCTTCTTCT 196
QY 288 CCTACATTTCTCACTCCCTCTCTCTAGTTTACTTAGCATGCGCGTCTTACTGGTTTT 347
Db 197 AATACATTCCAATTTCTCCCTGCTCTCTAGCTACTTAGCTTGGCCCTTTACTGGTTCT 256
QY 348 GCCAATCTTGCATCTCTCACTGGTTTATGGTCTCTCGGCATGAAATGGGCCATCATGCT 407
Db 257 GTCAAGCTAGCATCTCTCACTGGTTTATGGATCTCTCGGTCTATGAAATGGGTCAACCAT 316
QY 408 TTAGTGATACAGTGGATTCGATTAACGCGGTTGGATTCGCTCTCAATTCGGCTCTCTCTCA 467
Db 317 TTAGCGAGTACCAATGGGTTGACGCACTGTGGGCTTCATGCTCACTCATTTCTTCTCA 376
QY 468 CCCCTTACTTTTCTTGGAAATACAGCCATCCGAAAGCACCATGCAAAACACAAATTCACCT 527
Db 377 CTCCTTACTTCTTGGAAATACAGTACAGGAATCACCATGCCCAACAAAGTTCCATTG 436
QY 528 AAAACGAGGAAGTTTACATCTTAGAATCTAGTCCAGCTCAGGATCTTACTCCACATAG 587
Db 437 ATAACGATGAAGTTTACATCTTAAGAGCAAGTCCAACTCGCTCTT-----ACCTATA 490
QY 588 AATTTCTTGACACACGCGCTGTCGAATCTCTTGGTCTCATCTGTTTAACTTTAGGAT 647
Db 491 AGCTTCTTAAACACCTCCAGGAAGGCTGTTAGTTATGTTATCATGTTTCAACCTTAGAT 550
QY 648 TTCCTTTATACCTCTTAAACGAATGTTTCAGGCAAGAAGTACGATAGATTTCACCAACCACT 707
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QY 708 TTGATCCATTTGAGCCCGATCTTCCAGCGCTGAGCGAATCCAGGTTGGGTTTATCAGATC 767
Db 611 TCGACCCCATGATCCCAATTTTCAAGGAACGCTGAGAGGTTTTCAGGCTTGTCTTCTGATC 670
QY 768 TTGGTATCGTTGCAGTGTTTTACCGGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTT 827
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model  
Run on: September 24, 2006, 23:05:00 ; Search time 294 Seconds  
(without alignments)  
8948.228 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
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Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	870	61.9	1364	2	US-08-872-302-3	Sequence 3, Appli
2	657.6	46.8	1312	3	US-09-059-769-3	Sequence 3, Appli
3	640.4	45.5	1358	3	US-09-059-769-1	Sequence 1, Appli
4	611.2	43.5	1128	3	US-09-161-994A-1	Sequence 1, Appli
5	426.2	30.3	1372	3	US-09-133-962A-1	Sequence 1, Appli
6	426.2	30.3	1372	3	US-09-763-331-5	Sequence 5, Appli
7	426.2	30.3	1372	3	US-09-697-379-1	Sequence 1, Appli
8	426.2	30.3	1372	3	US-10-116-212A-1	Sequence 1, Appli
9	424.6	30.2	2973	3	US-09-133-962A-15	Sequence 15, Appl
10	424.6	30.2	2973	3	US-09-697-379-15	Sequence 15, Appl
11	424.6	30.2	2973	3	US-10-116-212A-15	Sequence 15, Appl
12	419.4	29.8	1422	4	US-09-837-751-5	Sequence 5, Appli
13	417.2	29.7	1164	4	US-10-185-578-1	Sequence 1, Appli
14	417.2	29.7	1222	2	US-08-314-596-43	Sequence 43, Appl
15	417.2	29.7	1222	2	US-08-320-982-43	Sequence 43, Appl
16	417.2	29.7	1222	2	US-08-819-037-43	Sequence 43, Appl
17	417.2	29.7	1222	3	US-08-819-037-43	Sequence 43, Appl
18	417.2	29.7	1448	2	US-09-045-940-43	Sequence 39, Appl
19	417.2	29.7	1448	2	US-08-314-596-39	Sequence 39, Appl
20	417.2	29.7	1448	2	US-08-320-982-39	Sequence 39, Appl
21	417.2	29.7	1448	3	US-08-819-037-39	Sequence 39, Appl
22	415.4	29.5	1476	2	US-09-045-940-39	Sequence 1, Appli
23	412.4	29.3	1231	2	US-08-872-302-1	Sequence 44, Appl

24	412.4	29.3	1231	2	US-08-320-982-44	Sequence 44, Appl
25	412.4	29.3	1231	3	US-08-819-037-44	Sequence 44, Appl
26	412.4	29.3	1231	3	US-09-045-940-44	Sequence 44, Appl
27	408	29.0	1155	2	US-08-675-650B-1	Sequence 1, Appli
28	408	29.0	1426	3	US-09-133-962A-3	Sequence 3, Appli
29	408	29.0	1426	3	US-09-697-379-3	Sequence 3, Appli
30	408	29.0	1426	3	US-10-116-212A-3	Sequence 3, Appli
31	407	28.9	1369	3	US-09-133-962A-11	Sequence 11, Appl
32	407	28.9	1369	3	US-09-697-379-11	Sequence 11, Appl
33	407	28.9	1369	3	US-10-116-212A-11	Sequence 11, Appl
34	406.4	28.9	1155	3	US-09-354-231B-13	Sequence 13, Appl
35	406.4	28.9	1155	3	US-09-128-602B-13	Sequence 13, Appl
36	406.4	28.9	1155	3	US-09-995-297-13	Sequence 13, Appl
37	406.4	28.9	1155	4	US-09-771-904A-13	Sequence 13, Appl
38	405.2	28.8	1155	2	US-08-675-650B-5	Sequence 5, Appli
39	404.8	28.8	1155	3	US-09-354-231B-15	Sequence 15, Appl
40	404.8	28.8	1155	3	US-09-354-231B-17	Sequence 17, Appl
41	404.8	28.8	1155	3	US-09-128-602B-15	Sequence 15, Appl
42	404.8	28.8	1155	3	US-09-128-602B-17	Sequence 17, Appl
43	404.8	28.8	1155	3	US-09-995-297-15	Sequence 15, Appl
44	404.8	28.8	1155	3	US-09-995-297-17	Sequence 17, Appl
45	404.8	28.8	1155	4	US-09-771-904A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-08-872-302-3  
; Sequence 3, Application US/08872302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; TITLE OF INVENTION: Developing Seeds of Vernonia galamensis  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/872.302  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Majarian, William R  
; REGISTRATION NUMBER: P-41,173  
; REFERENCE/DOCKET NUMBER: BB-1084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-4926  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1364 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 103..1254  
US-08-872-302-3

Query Match 61.9%; Score 870; DB 2; Length 1364;  
Best Local Similarity 86.1%; Pred. No. 2.3e-229;

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Qy	120	AAGATCATGATATGGAAGGAGCGCCCGATTTGATCCGCGCCCAATTCCTGTTAAGTGATC	179								
Db	149	ATGATCAATAATAAGCAACGTCACCGGTTGATGCGGCACCAATTCCTCGTTAAGCGATC	208								
Qy	180	TAAAGAAAGCAATCCCTGCAATGCTTCGCGCGATCCGCGTCTGGTTCATCCTGCTACG	239								
Db	209	TAAAGAAAGCAATCCCTCGCAATGCTTCGCGCATCTGCGCATCCGTTTCATCGTCTACG	268								
Qy	240	TAGTTTCAGATCTCATATACCTTCCTTTTATACACGGTCGCAACACCTACATTCCTC	299								
Db	269	TGTTTCAGATCTCATATATACCTTCCTTTTATACACGCTCGCAACCTTCATATTCCTC	328								
Qy	300	ACCTCCCTCCTCCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTGGCAATCTTGCA	359								
Db	329	TTCCTCCTCCTCCTCTACCTTACTTAGCATGCGCGTTTACTGGTTTGGCAATCTTGCA	388								
Qy	360	TCCTCAGCTGTTATGGTCTCTGCGCCATGAATGCGGCCATCATGCTTTAGTAGTAC	419								
Db	389	TCCTCAGCTGTTATGGTCTCTGCGCCATGAATGCGGCCATCATGCTTTATAGTAGTAC	448								
Qy	420	AGTGGATTGATTAACCGCTGCTGCTCCTCCATTGCGCTCTCCTCACCCTTACTTTT	479								
Db	449	AGTGGATTGATTAACCGCTGCTGCTCCTCCATTGCGCTCTCCTCACCCTTACTTTT	508								
Qy	480	CTTGGAAATACAGCCATCGAAAGCAACCATGCAAAACACAAATTCCTCGAAACGAGGAG	539								
Db	509	CTTGGAAATACAGCCATCGAAAGCAACCATGCAAAACACAAATTCCTCGAAACGAGGAG	568								
Qy	540	TTTACATTCCTAGAACTCAGTCCGACGTCAGGACTTACTCTCCACATACGAATTTCTGACA	599								
Db	569	TTTACATTCCTAGAACTCAGTCCGACGTCAGGACTTACTCTCCACATACGAATTTCTGACA	628								
Qy	600	ACAGCCCTGGTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	659								
Db	629	ACAGCCCTGGTGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	688								
Qy	660	TCTTAACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTGATCCATTTGA	719								
Db	689	TCTTAACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTGATCCATTTGA	748								
Qy	720	GCCGATCTTACCGAGCGTGAGCAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTG	779								
Db	749	GCCGATCTTACCGAGCGTGAGCAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTG	808								
Qy	780	CAGTGTGTTTACGAGTCAAGTTTCTGTACAAACAAAGGATTTGCTGGTGGTGTGCA	839								
Db	809	CTGTGTTTACGAGTCAAGTTTCTGTACAAACAAAGGATTTGCTGGTGGTGTGCA	868								
Qy	840	TGTATGAGGTTCCAGTGTAGTCTGAAATTCCTTCAATTCGTAAATCACTTATCTGCACC	899								
Db	869	TGTATGAGGTTCCAGTGTAGTCTGAAATTCCTTCAATTCGTAAATCACTTATCTGCACC	928								
Qy	900	ACACATCTGTGTCACCCATTAAGATTAACCGAATGGAACCTGGATCAAGAGGCT	959								
Db	929	ACACATCTGTGTCACCCATTAAGATTAACCGAATGGAACCTGGATCAAGAGGCT	988								
Qy	960	TCACCAATCGACAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1019								
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Qy	1140	CAATGTGAGAGGAGGCGCAAGGATGCAATTTACATCGAGCAAGTACGACACCAAGCACA	1199								
Db	1169	CAATGTGAGAGGAGGCGCAAGGATGCAATTTACATCGAGCCAGATGCAATGATAGACACA	1228								

Qy	1200	AAGGACATATTGTTACCATATAAATGTAATCGATGATG	1237								
Db	1229	AAGGTGATATTGTTACCATATAAATGTAATCGAGCTG	1266								
RESULT 2											
US-09-059-769-3											
; Sequence 3, Application US/09059769											
; Patent No. 6329518											
GENERAL INFORMATION:											
APPLICANT: Green, Allan											
APPLICANT: Singh, Surinder											
APPLICANT: Lenman, Marit											
APPLICANT: Stymne, Sten											
TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses											
TITLE OF INVENTION: Therefor											
NUMBER OF SEQUENCES: 20											
CORRESPONDENCE ADDRESS:											
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.											
STREET: 5370 Manhattan Circle, Suite 201											
CITY: Boulder											
STATE: Colorado											
COUNTRY: US											
ZIP: 80303											
COMPUTER READABLE FORM:											
MEDIUM TYPE: Floppy disk											
COMPUTER: IBM PC compatible											
OPERATING SYSTEM: PC-DOS/MS-DOS											
SOFTWARE: Patent in Release #1.0, Version #1.25											
CURRENT APPLICATION DATA:											
APPLICATION NUMBER: US/09/059,769											
FILING DATE: April 14, 1998											
PRIOR APPLICATION DATA:											
APPLICATION NUMBER: AU P06223											
FILING DATE: 15-APR-1997											
APPLICATION DATA:											
APPLICATION NUMBER: AU P06226											
FILING DATE: 15-APR-1997											
PRIOR APPLICATION DATA:											
APPLICATION NUMBER: US 60/043706											
FILING DATE: 16-APR-1997											
PRIOR APPLICATION DATA:											
APPLICATION NUMBER: US 60/050403											
FILING DATE: 20-JUN-1997											
ATTORNEY/AGENT INFORMATION:											
NAME: Ferber, Donna M.											
REGISTRATION NUMBER: 33,878											
REFERENCE/DOCKET NUMBER:											
TELEPHONE: (303) 499-8080											
TELEFAX: (303) 499-8089											
INFORMATION FOR SEQ ID NO: 3:											
SEQUENCE CHARACTERISTICS:											
LENGTH: 1312 base pairs											
TYPE: nucleic acid											
STRANDEDNESS: single											
TOPOLOGY: linear											
MOLECULE TYPE: cdna											
ORIGINAL SOURCE:											
ORGANISM: Crepis sp.											
FEATURE:											
NAME/KEY: CDS											
LOCATION: 26..1147											
US-09-059-769-3											

Query Match		46.8%	Score	657.6;	DB	3;	Length	1312;	
Best Local Similarity		76.4%;	Pred.	No. 7.3e-171;					
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Db 131 CCACATTGCTTCAGCGCATCTGTCACTCCGCTCATCTTATTACGTTGTCAGGATCTCAT 190  
QY 257 ATCACCTTCTTTTATACAGGTCGCCACACCTACATTCCTCACCTCCTCTCTCTA 316  
Db 191 ATTGCCTACATCTTCTACTCTCTGTCGCAACACATATATCCCTAATCTCCCTCATCTCTA 250  
QY 317 GTTACTAGCATGGCGGTTTACTGGTTTGTGCAATCTTGTCACTCTCTCTCTATGG 376  
Db 251 GCCTACTAGCTGGCGGCTTACTGGTTCTGTCAAGCTAGGCTCTCTCTCTCTATGG 310  
QY 377 GTCTCGGCATGAATTCGGCCCATCATGCTTTAGTGTAGTACAGTGGATTTGATAAGCC 436  
Db 311 ATCTCGGCATGAATGTGTCCATCCATGCTATAGCAACTACACATGGGTGTACGACACT 370  
QY 437 GTTGGATTGCTCTCTCACTCGGCTCTCTCACTCCCTTACTTTCTTGGAAATACAGCAT 496  
Db 371 GTGGGCTTTCATCATCCATTCATTTCTCTCCCTCACCCGCTATTTCTTGGAAATACAGTAC 430  
QY 497 CGAAGCACATCGCAACACAAATTCACCTCGAAACGAGAAAGTTTACATTTCTAGAACT 556  
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QY 557 CAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACGCTCGTGAATC 616  
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QY 737 COTGAGCGAATCCAGGTTCGGTTATCAGATCTTGGTATCTGTCAGTGTTCACGAGCT 796  
Db 665 COTGAGCGGTTTCAGTCTCTCTTTCGGATCTTGGTCTTCTTCTGCTGTTTATGGAAT 724  
QY 797 AGTTTCTTGTACAAACAAAGATTTGGTTGGTGTATGTCATGATGATGAGTTCAGTG 856  
Db 725 AAAGTTGCTGTAGCAATAAAGAGCTGCTTGGGTGGCTGATGATGATGAGTTCGCGTG 784  
QY 857 ATAGGTCTCAATTTCTTCAATTTATCGTAATCACTTATCTGCACACACATCTGCTCA 916  
Db 785 CTAGGCGTATTTACCTTTTTCGATGTGATCAGTTCTTACACACACCATCAGTCTGCG 844  
QY 917 CCCCATTACGATTTCAACCGAATGGAACTGGATCAAGAGGCTTTCACCAATTCGACAGA 976  
Db 845 CCTCATATGATTTCACTGAATGGAATGGATCAGAGGGCTTGTACGAATCGATAGN 904  
QY 977 GATTCGGTCTCTGATTCGGTTTTCAGAGGTTTACACACCCAGCTGTGACCAT 1036  
Db 905 GACTTTGGGTTCTGAAATAGTGTTCATGATGATGATGATGATGATGATGATGATGAT 964  
QY 1037 TTGTTTCCCTACATTCACATTCATCATGCAAGGAGGCAAGGCGGCAATCAAGCAATC 1096  
Db 965 TTGTTTTCATATTCACATTCATCATGCAAGGAGGCAAGGCGGCAATCAAGCAATC 1024  
QY 1097 TTGGGTGATTTACAGATGATTCAGAGGACTTCCATTTTTCAAAGCAATGTGGAGAGGCG 1156  
Db 1025 TTGGGCGACTTTTATATGATGATAGTACTCCATTTTAAAGCAATGTGGAGAGGCG 1084  
QY 1157 AAGGAATGATTTATATGAGCAAGATGAGAGCAAGCAAGCAAGCAATTTGGTAT 1216  
Db 1085 AGGGAATGATGATATATGAGCAAGCAAGCAAGCAAGCAAGCAATTTGGTAT 1138  
QY 1217 CATAAATGTAATC 1230  
Db 1139 CATAAATGTAATC 1152

RESULT 3  
US-09-059-769-1  
; Sequence 1, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Symme, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1358 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 30..1151  
; US-09-059-769-1  
  
Query Match 45.5%; Score 640.4; DB 3; Length 1358;  
Best Local Similarity 75.5%; Pred. No. 4.1e-166;  
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;  
  
QY 137 GAACGAGCCCGATTCGCGGCGCATTCCTGTTAAGTGAATCTAAAGAAAGCAATCCCT 196  
Db 75 GAACGTGTCTCAGTTGATTCAGTAACCTTCTCAGTGAATTCGAGCAAGCAATCCCT 134  
QY 197 GCACATTGCTTCGGCGGATCCGCCGCTGCTGCTCACTGCTAGTTCAGATCTCAT 256  
Db 135 CCCCATTGCTTCAGAGATCTGTAATCCGCTCATCTTACTATGTTGTTCAAGATCTCAT 194  
QY 257 ATCACCTTCTTTTATACAGGTCGCCACACCTACATTCCTCACCTCCTCTCTA 316





Db 719 GCGCGCGCTGGGTGACGTCATTTACGGAATCCAGTTTATAGCGGTGTTTATCTTTTCG 778  
Qy 879 TCGTAATCACTTATCTGCACACACACATCTGTGTCGTCACCCATTACGATTCAACCGAAT 938  
Db 779 ATATCATCACTTACTTGCACACACACCCATCTGTGTCGTCATATATGATTCATCTGAAT 838  
Qy 939 GGAATCGGATCAAAAGGAGCTTGCACACCAATCGACAGAGATTCGGTCTCTGGAATCGGG 998  
Db 839 CGAATCGGCTCAGAGGGGCTTTGTCAACATCGATAGGAGCTTGGGTTCTCTGAATAGTG 898  
Qy 999 TTTTCCACACGCTTACACACACCCAGGTGTGTCACCAATTTGTTCCCTACATTCACATTT 1058  
Db 899 TGTCTCATGATGTTACACACATCTCACTGTTATGCATCATCTGTTTTCATACATTCACACT 958  
Qy 1059 ATCATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1118  
Db 959 ATCATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1018  
Qy 1119 ACAGGACTCCATTTTCAAGCAATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
Db 1019 ATAGGACTCCATTTCTGAAAGCAATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078  
Qy 1179 AGATGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1228  
Db 1079 CTGAAAGAGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1128

## RESULT 5

US-09-133-962A-1

; Sequence 1, Application US/09133962A

; Patent No. 6372965

; GENERAL INFORMATION:

; APPLICANT: JONATHAN EDWARD LIGHTNER

; TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID

; DELTA-12 DESATURASES AND RELATED

; ENZYMES FROM PLANTS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

; SOFTWARE: MICROSOFT WORD VERSION 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/133,962A

; FILING DATE: 14-Aug-1998

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 07/977,339

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHRISTENBURY, LYNN M.

; REGISTRATION NUMBER: 30,971

; REFERENCE/DOCKET NUMBER: BB-1043-D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302)992-5481

; TELEFAX: (302)773-0164

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1372 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Arabidopsis thaliana

; IMMEDIATE SOURCE:

; CLONE: p92103

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 93..1244

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-133-962A-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372;

Best Local Similarity 61.0%; Pred. No. 4.le-107;

Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGAATGTCGGGATTCATATGATGATGATGATGATGATGAT 124  
Db 84 TCCAGAAATCATGGGTGCGAGGTGGAAGATGCGGGTTCCTACTTCTTCCAGAAATCGGAA 143  
Qy 125 CATGATATGGACGAAACGAGCCCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 184  
Db 144 ACCGACACCAAAAGCGGTGCGGTGCGGAGAAACCGCCCTTCTCGGTGGGAGATCTGAAG 203  
Qy 185 AAAGCAATCCCTGACATGTTTCCGGCGATCCGGCGGTCTGCTCATCTCTGCTACGTAGTT 244  
Db 204 AAAGCAATCCCGCGCATTTGTTTCAACGCTCAATCCCTCGCTCTTCTCTTACCTTATC 263  
Qy 245 CAGGATCTCATTCACCTTCTCTTTTATACGGTGCACCAACACCTTACATTCCTCACCTC 304  
Db 264 AGTGACATCATATAGCCTCATGCTTCTACTAGTCGCCCAACCAATTACTTCTCTCTCTC 323  
Qy 305 CCTCTCTCTCTAGTTTACTTTAGCATGGCGGTTTACTGGTGTGTTTGGCAATCTTGCATCTC 364  
Db 324 CCTCAGCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGCTCTA 383  
Qy 365 ACTGTTATGGGTCTCGGCCATGAATGCGGCCATCATGCTTGTAGTGAGTACGATGG 424  
Db 384 ACTGGTATCTGGGTCTATAGCCCAAGATCGGTGTCACGACATTCAGCGACATACCAATGG 443  
Qy 425 ATTGATAAGCGGTGGATTCTGCTCCATTCGGCTCTCCTCACCCCTTACTTTCTCTG 484  
Db 444 CTGGATGACACAGTTGGTCTTATCTTCCANTCTTCTCTCTCTCTCTCTCTCTCTCTCT 503  
Qy 485 AAATACAGCCATCGAAAGCACCACCAATTCATCGAAACAGGAAAGTTTAC 544  
Db 504 AGTATAGTCATCGCGGTGTCACCATTCACCACTGGATCCCTCGAAAGAGATGAAGTATT 563  
Qy 545 ATTCCTAGAACTCACTCCAGCTCAGGACTTACTCCACATAGCAATTTCTTGACAAACAG 604  
Db 564 GTCCCAAGCAGAAATCAGCAATCAAGTGGTACGGGAAATAC-----CTCAACACCCCT 617  
Qy 605 CTGTGTGNAATCTCATCTTGTGTCATCATGTTAACTTAGGATTTCTTTTATACCTTTA 664  
Db 618 CTGGACGCATCATGATGTTAACTTAACTTGTCTGCGGTGGCCCTTGTACTTAGCC 677  
Qy 665 ACGAATGTTTTCAGCAAGAGTACGATAGATTATCAACACCTTTGATCCATTTAGCCCG 724  
Db 678 TTTAAGCTCTTGGCAGACCGGTATGACGGGTGCGTGGCAATTTCTTCCCAACCGTCCC 737  
Qy 725 ATCTTTCACCGAGCGTGAGGAAATCCAGGTGCGGTATTCAGATCTTGGTATCGTTGAGTG 784  
Db 738 ATCTACAATGACCGAGAACCGCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCGTC 797  
Qy 785 TTTTACGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTGGTGGTGGTGGTGGTGGT 844  
Db 798 TGTTTTGGTCTTTTACCGTTACCGTCTGTCACAAAGGAGTGGCTCGATGATCTGCTCTAC 857  
Qy 845 GGAGTTTCCAGTGTAGGTCTGAAATTCCTTCAATTCATTCATTCATTCATTCATTCATTC 904  
Db 858 GGAGTACCGCTCTGATAGTGAATGGTTCCTCGTCTGATGATGATGATGATGATGATGAT 917  
Qy 905 CATCTGTCTCACCCCATTTACGATTTAACCGAATGGAATGGAATCAAGAGACGCTTGACC 964

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Db 918 CATCCCTGTTGGCTCACTACGATTCATCAGATGGGACTGGCTCAGGGAGCTTTGGCT 977
Qy 965 ACAATCGACAGAGATTTCCGGTCTCTGAAATCGGGTTTTCCACGAGCTTTACACACACCCAC 1024
Db 978 ACCGTAGACAGAGACTACGGAACTTTGAAACAGGTGTTCCACAACTTACAGACACACAC 1037
Qy 1025 GTGTTGCAACCAATTTGTTTCCCTACATTCACATTAATCATGCAAAAGGAGCAAGGAGGCC 1084
Db 1038 GTGGCTCATACCTGTTCTCGACAAATGCGCATTAATAACGCAATGGAAGCTTACAAAGGCG 1097
Qy 1085 ATCAAGCAAACTTTGGGTGATTCAGGATGATCGACAGGACTCCATTTTTCAAAGCAATG 1144
Db 1098 ATAAAGCCAAATTTCTGGGAGACTATTACCAAGTTCCGATGGAACACCGTGTGTATGTAGCGGATG 1157
Qy 1145 TGGAGAGAGGCAAGGAATGCAATTTACATCGAGCAAGATGCAAGCAGCAGCAAGCAAGAGG 1204
Db 1158 TATAGGAGGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1217
Qy 1205 ACATATTGGTACCAATAAATGTAAT 1229
Db 1218 GTGTACTGGTACAAATAAGTTAT 1242

RESULT 6
US-09-763-331-5
; Sequence 5, Application US/09763331
; Patent No. 6825335
; GENERAL INFORMATION:
; APPLICANT: Martin, Charles E.
; APPLICANT: Mitchell, Andrew
; TITLE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for
; FILE REFERENCE: 97-0081 PCT
; CURRENT APPLICATION NUMBER: US/09/763,331
; PRIOR FILING DATE: 1999-08-24
; PRIOR FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: SeqSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1372
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-763-331-5

Query Match 30.3%; Score 426.2; DB 3; Length 1372;
Best Local Similarity 61.0%; Pred. No. 4.1e-107;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTCATATGATGATCGAATGAAAGAT 124
Db 84 TCCAGAAACATGGGTGCGAGGTGGAAGATGCGGTTCTCTACTTCTTCCAGAAATCGGAA 143
Qy 125 CATGATATGGAGCAAGACGAGCCCGCATGATGATCGGCGCCATTTCTGTTAAGTATCTAAAG 184
Db 144 ACCGACACACAAAGCGGTGTCGGTGCAGAAACCGCCTTTCTCGGTGGGAGATCTGAAG 203
Qy 185 AAAGCAATCCCTGACATGTTCTCGGCGATCCGCGCTGTGTCATCTGCTACGATGTT 244
Db 204 AAAGCAATCCCGCCGATGTTTTCAAAGCTCAATCCCTCGCTCTTTCTCTACCTTATC 263
Qy 245 CAGGATCTCATTCATCCTCTCTTTTATACAGGTCGGCAACACCTACATTCCTCACCTC 304
Db 264 AGTGACATCATTTATAGCTCATGCTTCTACTAGTCGCAACCAATTAATCTCTCTCTC 323
Qy 305 CCTCTCTCTAGTTTACTAGCATGGCGGTTTACTGTTTGGCAATCTTTGCAATCTCTC 364
Db 324 CCTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGTCTCTA 383
Qy 365 ACTGGTTTATGGTCTCGGCCATGATCGGCCATCATGCTTTAGTGAGTACCAGTGG 424
Db 384 ACTGGTATCTGGGTCAATAGCCCAAGAAATCGGTACCAAGCAATTCAGGCAATTCACCAATGG 443
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Qy 425 ATTGATAACGCGGTGGAATTCGTCCTCATTCGGCTCTCTCACCCCTTACTTTTCTTGG 484
Db 444 CTGATGACACAGTTGGTCTTATCTTCCATTCCTTCTCTCGTCCCTTACTTCTCTGG 503
Qy 485 AATACAGCCATCGAAGAGCAGCAATGCAAAACACAAATTCACTCGAAAACGAGGAAGTTTAC 544
Db 504 AAGTATAGTATCGCCGTCCACATTCACACATCGATCCCTCGAAGAGATGAAGTATTT 563
Qy 545 ATTCCTAGAACTCAGTCCCGAGCTCAGGACTTACTCCACATACGAAATTTCTTTGACAAACAG 604
Db 564 GTCCAAAGCAGAAATCAGCAATCAAGTGTACGGGAATAC-----CTCAACAACCTC 617
Qy 605 CTGGTTCGAATCTCATCTTGGTTCATGTTAACTTAGGATTTCTTTATACCTCTTA 664
Db 618 CTGGAGCGCATCATGATGTTAAACCGTCCAGTTTGTCTCGGGTGGCCCTTTGTACTTAGCC 677
Qy 665 ACGAATCTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTTGATCCCATTCGAGCCG 724
Db 678 TTTAACGTCTCTGGCAGACCGGTATGACGGTTCGCTTGCCATTTCTTCCCAACGCTCCC 737
Qy 725 ATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTCAGTGT 784
Db 738 ATCTACATGACCGAGAACGCTCCAGATATACCTCTCTGATCGGGTATTTCTAGCCGTC 797
Qy 785 TTTTACGGAATCAAGTTTCTGTACAAACAAAGGATTTGGTTGGGTGATGTGATGTAT 844
Db 798 TGTTCGTCCTTTACCGTTACCGTCTGTCACAAAGGATGCGCTCGATGATCTGCTCTAC 857
Qy 845 GGAGTTCAGTATAGTCTGAAATTCCTCATTTATCGTAACTTATCTGACCAACACA 904
Db 858 GGAGTACCGCTTCTGATAGTAAATGCGTTCCTCTGATGATCACTTACTTTGACGACACT 917
Qy 905 CATCTGTCGTCACCCCATTTACGATTTCAACCGAATGGAATCGGATCAAGGAGCCTTGACC 964
Db 918 CATCCCTGTTGCTCTACTAGATTCATCAGATGGGACTGGCTCGCTCAGGGAGCTTTGGCT 977
Qy 965 ACAATCAGACAGATTTCCGGTCTCTGAAATCGGGTTTTTCCACGAGCTTTACACACACCCAC 1024
Db 978 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACAACTTACAGACACACAC 1037
Qy 1025 GTGTTGACCAATTTGTTTCCCTACATTCACATTCATTCGAAAGGAGGCAAGCGGCC 1084
Db 1038 GTGGCTCATCACCTGTTCTCGACAAATGCGCATTAATAACGCAATGGAAGCTTACAAAGCG 1097
Qy 1085 ATCAAGCAATCTTGGGTGATTCAGGATGATCAGAGGATTCAGACAGGACTCCATTTTTCAAAGCAATG 1144
Db 1098 ATAAAGCCAAATCTGGGAGACTATTACCAAGTTCCGATGGAACACCGTGTGTATGTAGCGATG 1157
Qy 1145 TGGAGAGAGGCAAGGAATGCAATTTACATCGAGCAAGATGCAAGCAGCAGCAAGCAAGAGG 1204
Db 1158 TATAGGAGGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1217
Qy 1205 ACATATTGGTACCAATAAATGTAAT 1229
Db 1218 GTGTACTGGTACAAATAAGTTAT 1242
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RESULT 7
US-09-697-379-1
; Sequence 1, Application US/09697379
; Patent No. 6872872
; GENERAL INFORMATION:
; APPLICANT: JONATHAN EDWARD LIGHTNER
; APPLICANT: JOHN JOSEPH OKULEY
; TITLE OF INVENTION: GENES FOR MICROSOMAL
; DESATURASES AND RELATED
; ENZYMES FROM PLANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
```

STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Microsoft Word Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/697,379  
FILING DATE: 26-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M..  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: B01043 US DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 835420

## INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1372 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana

IMMEDIATE SOURCE:

CLONE: p92103

FEATURE:

NAME/KEY: CDS

LOCATION: 93..1244

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-697-379-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372; .

Best Local Similarity 61.0%; Pred. No. 4.1e-107;

Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

QY	65	TTCCAGAAATCTGGGAGAGTAGCAGAAATCTCGGATTTCATATGATGATCGAATGAAAGAT	124
DB	84	TCAGAAACATGGTGCAGGTGGAAGATGCCGGTCTCTACTTCTTCCAGAAATCGGAA	143
QY	125	CATGATATGGACGACGAGCCCGATTGATCCGGCGCCATTCCTGTTAAAGTGATCTAAAG	184
DB	144	ACCGACACCAACGAGCGTGTCCGTCGAGAAACCGCTTCTCGGTGGGAGATCTGAAG	203
QY	185	AAAGCAATCCCTGCAATTGCTTCCGGCGATCCGGCTCTGGTCATCTCTGCTACGTAGT	244
DB	204	AAAGCAATCCCGCGCATTTGTTTCAAAACGCTCAATCCCTCGCTCTTCTCTCTACCTATC	263
QY	245	CAGGATCTATATACCTTCTTTTATACAGCTCGCCAGACCTACATTCCTCTACCTC	304
DB	264	AGTGACATCATATAGCCTCATGCTTCTACTAGCTGCGCAACCAATTACTTCTCTCCTC	323
QY	305	CTCTCTCTCTTACTTACTAGCATGCGCGTTTACTGTTTTCGCAATCTTGCATCTCTC	364
DB	324	CTCAGCCTCTCTTACTTGGTGGCCACTATTTGGCCCTGTCAAGCTGTGTCTTA	383
QY	365	ACTGGTTTATGGTCTCGGCCATGAATGGCGCATCATGCTCTTTAGTGAGTACGAGTGG	424
DB	384	ACTGGTATCTGGTCTATAGCCCAAGATGCGGTCAACGATTCAGCGACTACCAATGG	443

QY	425	ATTGATAACGCGGTTGGATTTCCTCTCCATTCCGGCTCTCTCACCCCTTACTTTTCTTGG	484
DB	444	CTGGATGACACAGTTGGTCTTATCTTCCATTCTCTCTCTCTCTCTCTCTCTCTCTGG	503
QY	485	AAATACAGGCATCGAAAGCACCATCGAACAACAAATTCACTCGAAACAGGAAAGTTAC	544
DB	504	AAATATAGTCATCGCGCTGACCAATTCACACTGGATCCCTCGAAAGAGATGAAGTATTT	563
QY	545	ATTCTAGAACTCAGTCCCGCTCAGGACTTACTCCATACAGAAATTTCTTGACACACG	604
DB	564	GTCCCAAGCAGAAATCAGCAATCAAGTGTACGGGAATAC-----CTCACAACCT	617
QY	605	CCTGGTCGAATCCTCATCTTGGTCATCATGTTAACTTAGGATTTCTTTTACCTTTA	664
DB	618	CTTGACGCTCATGATGTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT	677
QY	665	ACGAATGTTTCAAGCAAGTACGATAGATTTACCAACCACTTTGATCCATTTAGCCCG	724
DB	678	TTTAAAGTCTCTGGCAGACCGTATGACGGTTTGGTTCCTTCCCAACCGCTCTAC	737
QY	725	ATCTTACCGAGCTGAGCAATCCAGGTTCGGTTTACAGATCTTGGTATCGTTGAGTG	784
DB	738	ATCTAATGACCGAGACCGCTCCAGATATACCTCTCTGATCGGGTATTTCTAGCCGTC	797
QY	785	TTTTACGACTCAAGTTTCTTGTAACAAACAAAGGATTTGGTGGGTGATGTGATGTAT	844
DB	798	TGTTTTGGTCTTTACCGTTACGCTGTCGACAAAGGATGGCTCGATGATCTGCTCTAC	857
QY	845	GGAGTTCAGTATAGTCTGAATTCCTTCAATTCATTCATCTTCTGATCGGGTATTTCT	904
DB	858	GGAGTACCGCTTCTGATAGTGAATGGTTCCTCTGATCACTTACTTCTGAGCACT	917
QY	905	CATCTGTGTCACCCCATTTACGATTCACCGCAATGGAATCGGATCAAGAGAGCTTGACC	964
DB	918	CATCCCTCTGCTCCTCATACGATTCATCAGAGTGGGCTGGCTCAGGAGAGCTTTGGCT	977
QY	965	ACAATCGACAGAGATTTTCGGTCTCTCGAATCGGGTTTTCACGAGCTTACACACCCAC	1024
DB	978	ACCGTAGACAGAGACTACGGAATCTTGAACAAAGTGTTCACACAACTTACAGACACAC	1037
QY	1025	GTGTTGACCATTTGTTTCCCTACATTCACATTCATGCAAGAGGCAAGAGGCGG	1084
DB	1038	GTGGCTCATCACTGTTCTCGCAATGCGCATTTAAGCGAATGGAAGCTTCAAGAGCG	1097
QY	1085	ATCAAGCCAATCTTGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATG	1144
DB	1098	ATAAGCCAATTTCTGGGAGACTTATACAGTTTCGATGGAAACCCGTTGGTATGTAGGATG	1157
QY	1145	TGGAGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGACAGACGCAAGAGG	1204
DB	1158	TATAGGAGGCAAGAGGTGATCTTATGTAGAACCGGACAGGAGGTGCAAGAAAGT	1217
QY	1205	ACATATGCTACATAAATGTAAT	1229
DB	1218	GTGTACTGTACAACTAAGTTAT	1242

## RESULT 8

US-10-116-212A-1

; Sequence 1, Application US/10116212A

; Patent No. 6919466

; GENERAL INFORMATION:

; APPLICANT: JONATHAN EDWARD LIGHTNER

; JOHN JOSEPH OKULEY

; WILLIAM DEAN HITZ

; ANTHONY JOHN KINNEY

; NARENDRA YADAV

; LUIS PEREZ-GRAU

; TITLE OF INVENTION: GENES FOR MICROSOMAL

; FATTY ACID DELTA-12

; DESATURASES AND

; HYDROXYLASES FROM PLANTS

NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Dell  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: Microsoft Word 97 SR-2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,212A  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 09/697,379  
FILING DATE: 26-OCT-2000  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998  
APPLICATION NUMBER: U.S. 08/262,401  
FILING DATE: 20-JUN-1994  
APPLICATION NUMBER: PCT/US93/09987  
FILING DATE: 15-OCT-1993  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB1043USDIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 835420

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1372 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: p92103  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..1244  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-116-212A-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372;  
Best Local Similarity 61.0%; Pred. No. 4.1e-107;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;  
QY 65 TTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTTCATATGATCGATGAAAGAT 124  
DB 84 TCAGAAACATGGGTGCGAGGTGGAGAAATGCGGGTTCCTTCTTCCAGAAATCGGAA 143  
QY 125 CATGATATGGACGAAACGAGCCCGGATTGATCCGGCCCATTCCTCGTTAAGTGATCTAAAG 184  
DB 144 ACCGACACCAAAAGCGGTGCGGTGCGAGAAACCGCCCTTCTCGGTGGAGATCTGAAG 203  
QY 185 AAAGCAATCCCTGCAATTGCTTCGGGGATCCGGCGTCTGTGTCATCTCTGCTACGTAGTT 244  
DB 204 AAAGCAATCCCGCCGCAATGTTTCAACGCTCAATCCCTCGCTCTTTCTCTACCTTATC 263  
QY 245 CAGGATCTCATTTACCTTCTTTTATACACGGTCGCCAACACCTACATTCCTCACCTC 304

DB 264 AGTGACATGATTATAGCCTCATGCTTCTACTAGTCCGCCACCAATTACTTCTCTCTCCTC 323  
QY 305 CTTCTCTCTTAGTTTACTTAGCAATGCGCGTTTACTGGTTTGGCCAAATCTTGTGATCCTC 364  
DB 324 CTTGAGCCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGTCTCTA 383  
QY 365 ACTGGTTTATGGGCTCTCGGCCATGAATGGGCCATCATGCTTATAGTGTAGTACAGTGG 424  
DB 384 ACTGGTATCTGGGTATAGCCACGAATGGGTGTCACCAAGCATTCAGCGACTACCAATGG 443  
QY 425 ATTGATAACGCGGTTGGATTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 484  
DB 444 CTGATGACAGAGTTGGTCTTAICTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 503  
QY 485 AAATACAGCCATCGAAAGCACCATGCAAAACAAATTCATCTCGAAAAACGAGGAAGTTTAC 544  
DB 504 AAGTATAGTCAATCGCGCTCAACATTCACATGATCCCTCGAAAGAGATGAAGTATTT 563  
QY 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAAATTTCTTGACAACAG 604  
DB 564 GTCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACAAACCT 617  
QY 605 CTTGTCGAATCCTCATCTTGGTCACTGTTAACTTAGGATTTCTTTATACCTCTTA 664  
DB 618 CTGAGCGCATCATGATGTTAAACGCTCCAGTTTGTCTCTCGGTGGCCCTTGTACTTAGCC 677  
QY 665 ACGAATGTTTCAGCAAGAGTAGTAGATTTTACCAACCACTTTGATTCATTTGAGCCGG 724  
DB 678 TTTAAAGTCTCTGGCAGACCGTATGACGGGTTCTGTTGCCATTTCTTCCCAACGCTCC 737  
QY 725 ATCTTACCGAGCGTGAGCGAATCCAGTTGCGTTATCAGATCTTGTATGCTTGTGAGTG 784  
DB 738 ATCTTACCAATGACCGAGAACGCTCCGATATACCTCTCTGATCGGGGTATTTCTAGCCG 797  
QY 785 TTTTACCGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTTGGGTGATGTCATGTAT 844  
DB 798 TGTTTGGTCTTTACCGTTACGCTGCTGCACAGGGATGGCTCGATGATCTGCTCTAC 857  
QY 845 GGAGTTCCAGTGATAGGTCTGAAATTCCTTCAATATCGTAATCACTTATCTGCAACACAC 904  
DB 858 GGAGTACCGCTTCTGATAGTAGTGAATGCGTTCCTCTTGTATCACTTACTTTCAGCACAC 917  
QY 905 CATCTGTGTCACCCCATTAAGATTCAACGAAATGGAATGGATCGATCAAGAGAGCTTGACC 964  
DB 918 CATCCCTGTTGCTCTACATGATTCAGATTCAGAGTGGGACTGGCTCAGGGGAGCTTTGG 977  
QY 965 ACAATCGACAGAGATTTTCGGTCTCTGAAATCGGGTTTTTCCACGACGTTTACACACCCAC 1024  
DB 978 ACCGTAGACAGAGACTAGGNAATCTTGAACNAAGGTGTTCCACACATTTACAGACACAC 1037  
QY 1025 GTGTTGCAACATTTGTTTCCCTCAATTCACATTCATCATGCAAGAGGAGGAGGAGGCC 1084  
DB 1038 GTGGCTCATCACCTGTTCTCGACAAATGCGCATTTATAACGCAATGGAAGCTTACAAAGCG 1097  
QY 1085 ATCAAGCAATCTTGGGTGATTACAGGATGATCGACAGGACTCCCATTTTCAAGCAATG 1144  
DB 1098 ATAAAGCAATTTCTGGGAGACTATTAACAGTTGATGGAACACCGTGGTATGTAGCGATG 1157  
QY 1145 TGGAGAGAGGCAAGGAATGCAATTTATCCAGCAAGATTCAGACAGCAGCAAGCAACAAAGG 1204  
DB 1158 TATAGGAGGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGACAGAAAGGT 1217  
QY 1205 ACATATGGTACCAATAAATGTAAT 1229  
DB 1218 GTGTAAGTACCAATAAGTTAT 1242

## RESULT 9

US-09-133-962A-15  
; Sequence 15, Application US/09133962A  
; Patent No. 6372965  
; GENERAL INFORMATION:

APPLICANT: JONATHAN EDWARD LIGHTNER  
JOHN JOSEPH OKULEY  
TITLE OF INVENTION: GENES FOR MICROSMAL FATTY ACID  
DELTA-12 DESATURASES AND RELATED  
ENZYMES FROM PLANTS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/133,962A  
FILING DATE: 14-Aug-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNN M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1043-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)992-5481

TELEFAX: (302)773-0164

TELEX: 835420

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2973 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana

IMMEDIATE SOURCE:

CLONE: pAF2-6

FEATURE:

NAME/KEY: exon

LOCATION: 433..520

FEATURE:

NAME/KEY: intron

LOCATION: 521..1654

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-133-962A-15

Query Match 30.2%; Score 424.6; DB 3; Length 2973;  
Best Local Similarity 60.9%; Pred. No. 1.6e-106;  
Matches 710; Conservative 0; Mismatches 449; Indels 6; Gaps 1;  
65 TTCAGAAATCTGGGAGAGTACGAGAAATGTCGATTTCATATGATGATCGAATGAAAGAT 124  
1650 TGCAGAAACATGGGTGAGTGGAGAAATGCGGTTCTCTTCCAGAAATCGGAA 1709  
125 CATGATATGGAGCAAGCGCCGATTGATCGGCGCGATTCTCGTTAAGTATCTTAAG 184  
1710 ACCGACACCAAGAGCGTGGCGTCGAGAAACCCGCTTCTCGGTGGGAGATCTGAAG 1769  
185 AAAGCAATCCCTGCACATTGCTTCGCGGATCGCGGATCGCGTCTGTCATCTGCTACGTAGTT 244  
1770 AAAGCAATCCCGCGATTGTTTCAACGCTCAATCCCTCGCTCTTCTCTTACCTATC 1829  
245 CAGGATCTCATATCACTCTCTCTTTTATACCGGTGCCAACAACCTTACCTTCACTC 304

Db 1830 AGTGACATCATTTAGCCTCATGCTTCTACTAGTCGCCACCAATTACTTCTCTCTCTC 1889  
QY 305 CCTCTCTCTAGTTTACTTAGCATGGCCGTTTACTGGTTTGTGCAATCTTGTCAATCTC 364  
Db 1890 CCTCAGCCTCTCTCTTACTTGGCTTGGCCACTCTATTGGCCCTGTCAAGGCTGTCTC 1949  
QY 365 ACTGGTTTATGGTCTCTGGCCATGAATGGCCCATCATGCTTGTAGTGTACAGTGG 424  
Db 1950 ACTGGTATCTGGTTCATAGCCCAAGATGCGGTCCACCGCATTCAGCGCATACCA 2009  
QY 425 ATTGATAAGCGCGTTGGATTGCTCTCCATTCCTGCGGTCTCTTCAACCCCTTACTT 484  
Db 2010 CTGGATGACACAGTTGGTCTTATCTTCCATCTCTCTCTCTCTCTCTCTCTCT 2069  
QY 485 AAATACAGCCATCGAAAGCAACCATGCAACAAATCACTCGAAAGAGAGAGTATTAC 544  
Db 2070 AAGTATAGTCATGCGCGTCACCATTCCAACACTGGATCCCTCGAAAGAGATGA 2129  
QY 545 ATTCTAGAACTCAGTCCAGCTCCAGCTCAGGACTTACTCCATAGCAATTTCTTGAC 604  
Db 2130 GTCCCAAGACGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACA 2183  
QY 605 CTTGGTTCGAATCCTCATCTTGGTTCATGTTTAACTTAGGATTTCTTTTATACCT 664  
Db 2184 CTTGGACGATCATGATGTTAACCGTCCAGTTTCTCGGTGCGCCCTTGTACTTAGCC 2243  
QY 665 ACGAATGTTTCAGGCAAGAAGTACGATAGATTACCAACCACTTTTGATCCATTGAG 724  
Db 2244 TTTAAGCTCTCTGGCAGACCGTATGACGGTTTCTGCTTGCATTTCTTCCCAACG 2303  
QY 725 ATCTTACCGAGCGTGGAGGAATCCAGGTGGGTTTATCAGATCTTGGTATCGTTGCA 784  
Db 2304 ATCTACAATGACCGAGAAACGCTCCAGATATACCTCTCTGATGCGGGTATTCT 2363  
QY 785 TTTTACGGACTCAAGTTTCTGTACAAACAAAGGATTGTTGGTGTATGTCATGTAT 844  
Db 2364 TGTGTTGGTCTTTACCGTTACGCTGCTGCAAGGAGTGGCTCGATGATCTGCTCT 2423  
QY 845 GGAGTTCACGATGATAGGTCTGAAATTCCTTCAATTATCGTAATCACTTATCTGCA 904  
Db 2424 GGAGTACCGCTTCTGATAGTGAATGCTTCTCGTCTTGATCATTACTTGCAGCAC 2483  
QY 905 CATCTGCTCACCCCATTCAGATTCAACCGAATGGAATCGAATCAAGGAGCCTTGACC 964  
Db 2484 CATCCCTCGTTCCTCACTACGATTTCATCAGATGGGACTGGCTCAGGGAGCTTT 2543  
QY 965 ACAATCGACAGAGATTTCGCTCTCGTTCCTGATCGGTTTCCACGAGCTTACACA 1024  
Db 2544 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACACATTTACACA 2603  
QY 1025 GTGTTGCACCAATTTGTTTCCCTTACATTCACATTTATCGAAAGGAGGAGCGG 1084  
Db 2604 GTGGCTCATCCTCTGTTCTCGACATGCGCATTTATACGCAATGGAACCTACA 2663  
QY 1085 ATCAAGCCAAATCTGGGTGATTCAGGATGATTCGACAGACTTCCATTTTTCAAAG 1144  
Db 2664 ATAAAGCCAAATCTGGGAGACTATTACGATTTCGATGGAAACACCGTGTATGT 2723  
QY 1145 TGGAGAGGCGCAAGGATGCAATTTACATCGAGCAAGATGACAGACAGCAAGAGG 1204  
Db 2724 TATAGGGAGGCAAGAGGTGATCTATGTAGAACCGGACAGGGAAGGTGACAAG 2783  
QY 1205 ACATATTGTCATCAATAAATGTAAT 1229  
Db 2784 GTGTACTGTACACAAATAAGTTAT 2808

RESULT 10

US-09-697-379-15

; Sequence 15, Application US/09697379

; Patent No. 682872

; GENERAL INFORMATION:

; APPLICANT: JONATHAN EDWARD LIGHTNER







Patent No. 6919466  
GENERAL INFORMATION:  
APPLICANT: JONATHAN EDWARD LIGHTNER  
JOHN JOSEPH OKULEY  
WILLIAM DEAN HITZ  
ANTHONY JOHN KINNEY  
NARENDRA YADAV  
LUIS PEREZ-GRAU  
TITLE OF INVENTION: GENES FOR MICROSOMAL  
FATTY ACID DELTA-12  
DESATURASES AND  
HYDROXYLASES FROM PLANTS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Dell  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: Microsoft Word 97 SR-2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,212A  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 09/697,379  
FILING DATE: 26-OCT-2000  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998  
APPLICATION NUMBER: U.S. 08/262,401  
FILING DATE: 20-JUN-1994  
APPLICATION NUMBER: PCT/US93/09987  
FILING DATE: 15-OCT-1993  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB1043USDIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2973 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: pAF2-6  
FEATURE:  
NAME/KEY: exon  
LOCATION: 433..520  
FEATURE:  
NAME/KEY: intron  
LOCATION: 521..1654  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-116-212A-15

Query Match 30.2%; Score 424.6; DB 3; Length 2973;  
Best Local Similarity 60.9%; Pred. No. 1.6e-106;

	Matches	710;	Conservative	0;	Mismatches	449;	Indels	6;	Gaps	1;
QY	65	TTTCAGAAATCTGGAGAAAGTAGCAGAAATGTCGGATTTCATATGATGATCGAATGAAGAT	124							
DB	1650	TGCAGAAACATGGTGCAGTGAAGAAATGCCGGTTCCTACTTCTTCCAGAAATCGGAA	1709							
QY	125	CATGATATGGACGACGAGCCCGGATTGATCGGGGCCATTCCTGTTAAGTATCTAAAG	184							
DB	1710	ACCGACACCAAAAGCGTGCCTGCGAGAAACCGCTTCTCGGTGGAGATCTGAAG	1769							
QY	185	AAAGCAATCCCTGCACATTCCTTCGGCGATCCGCGTCTGGTTCATCTCTGCTACGTAGT	244							
DB	1770	AAAGCAATCCCGCGCATTTGTTTCAACGCTCAATCCCTCGCTCTTCTCTTACCTTATC	1829							
QY	245	CAGGATCTCATTTATCACCTTCTCTTTTATACCGGTGGCCAAACCTTACATTCCTCACCTC	304							
DB	1830	AGTGACATCATTTATAGCCTCATGCTTCTACTAGTGCACCAAAATTAATCTCTCTCTC	1889							
QY	305	CCTCTCTCTTAGTTTACTTAGCATGGCCGGTTTACTGTTTGTGCAATCTTGCATCTTC	364							
DB	1890	CCTCAGCCTCTCTTACTTTGGCCACTCTATTTGGGCCCTGTCAAGGCTGTGTCTTA	1949							
QY	365	ACTGGTTTATGGTCTCTCGGCCATGAATGCGGCCATCATGCTTTTATGAGTACAGTAGTG	424							
DB	1950	ACTGGTATCTGGGTATAGCCCAAGATCGGTACACGATTCAGCGACTACCAATGG	2009							
QY	425	ATTGATAACGCCGTTGGATTTCCTTCCATTCGGCTCTCTCACCCCTTACTTTTCTTGG	484							
DB	2010	CTGGATGACACAGTTGGTCTTATCTTCCATTCCTTCTCTCTCTCTCTCTCTCTCTG	2069							
QY	485	AAATACAGCCATCGAAAGCACCATGAAACAAATTCATCTGAAACAGAGAAAGTTTAC	544							
DB	2070	AAGTATAGTCATCGCGCTCACCATTCCAACTGGATCCCTCGAAAGAGATGAAGTATT	2129							
QY	545	ATTCTTAGAATCTAGTCCAGCTCAGGACTTACTCCACATAGCAATTTCTTGACACAG	604							
DB	2130	GTCCCAAGCAGAAATCAGCAATCAAGTGTGCGGAAATAC-----CTCAACACCCCT	2183							
QY	605	CCTGGTCGAATCCTCATCTTGGTTCATCATGTTAACTTAGATTTTCTTTATACCTCTTA	664							
DB	2184	CTTGGAGCATCATGATGTTAACCGTCCAGTTTGTCTCGGGTGGCCCTTGTACTTAGCC	2243							
QY	665	ACGAATGTTTTCAGGCAAGAGTACGATAGATTTCACACACTTTGATTCATTGAGCCCG	724							
DB	2244	TTTAACTCTCTGGCAGACCGTATGACGGTTTCGTTGCCATTTCTTCCCAACGCTCCC	2303							
QY	725	ATCTTACCGAGGTGAGGGAATCCAGTTGCGTTATCAGATCTTGATCGTTGTCAGTG	784							
DB	2304	ATCTAATGACCGAGAACGCTCCAGATATACCTCTCTGATCGGGTATTCTAGCCGTC	2363							
QY	785	TTTTACGGAATCAAGTTTCTGTACAAACAAAGGATTTGGTTGGGTGATGTGCATGTAT	844							
DB	2364	TGTTTTGGTCTTTACCGTTACGCTGCTGCAAGGATGCGCTCGATGATCTGCTCTAC	2423							
QY	845	GGAGTTCAGTATAGTCTGAAATTCCTTATTCGTTAATCATCTTATCTGCAACACACA	904							
DB	2424	GGAGTACCGCTTCTGATAGTGAATGGTTCCTCTGATCATCTTACTTTCAGACACACT	2483							
QY	905	CATCTGCTCACCCCATTTACGATTTCAACCGAATGGAATGGATCAAGAGGCTTGACC	964							
DB	2484	CATCCCTCGTCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	2543							
QY	965	ACAATCGACAGAGATTTCCGTTCTCCTGAATCCGGTTTTCACGACGTTTACACACCCAC	1024							
DB	2544	ACCGTAGACAGAGATCAAGGAATCTTGAACAAGGTGTTCCACAATTTACAGACACAC	2603							
QY	1025	GTGTTGCACCATTTGTTTCTTCCCTACATTCACATTTATCATGCAAGAGGCAAGCGGCC	1084							
DB	2604	GTGGCTCATCCTGTTCTCGACAAATGCGCATTTATAACGCAATGGAAGCTACAAAGCG	2663							
QY	1085	ATCAAGCCAAATCTGGGTGATTTACAGGATGATGACAGAGACTCCCATTTTCAAGCAATG	1144							
DB	2664	ATAAAGCCAAATCTGGGAGACTATTACAGTTTCGATGGAACACCGGTGATGTGGCGATG	2723							

QY 1145 TGGAGAGGCGCAAGGAATGATTTACATCGAGGAAGATGAGACAGCAAGCAACAGGG 1204  
Db 2734 TATAGGAGGCGCAAGGAATGATTTACATCGAGGAAGATGAGACAGCAAGGAAGT 2783  
QY 1205 ACATATTGGTACCATATAAATGTAAT 1229  
Db 2784 GTGTACTGGTACACAAATAGTTAT 2808

## RESULT 12

US-09-837-751-5  
; Sequence 5, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Gossypium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98)..(1246)  
US-09-837-751-5

Query Match 29.8%; Score 419.4; DB 4; Length 1422;  
Best Local Similarity 60.1%; Pred. No. 3,1e-105;  
Matches 718; Conservative 0; Mismatches 471; Indels 6; Gaps 1;  
QY 49 ATTTCTAATTTGGATTTTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTCAATAGA 108  
Db 73 ATCTCAATTTTAAAGGTTGGAACAATGGGTCTGGAGGAGAAATGTCGGTTCCAAACGAG 132  
QY 109 TGATCGAATGAAGATCATGATATGGACGAGACGCCGATGTGATCGGGCCCAATTCCTC 168  
Db 133 TCCAAAANAACCCGAATTCACCTCACTGAAGCGAGTTCCATCTCAAAAGCCACCCCTTCAC 192  
QY 169 GTTAAGTGTATCTAAAGAAGCAATCCCTGCACATTTGCTTCGGCGATCGCGCTCTGGTC 228  
Db 193 TCTGAGTGAATCAAGAAGACCATCCACCAACACTGTTTCAGCGCTCGTTTACGGCTC 252  
QY 229 ATCTCTGCTACGTTAGTTCAGGATCTCAATTATCACCTTCCTTTTATACAGCGTGCACAC 288  
Db 253 ATTTCTCATATCTCTTTAGGACTTTATATGGCTCTCTCTTTTATACCATGTGGCCACCAA 312  
QY 289 CTACATTCCTCACTCCCT 348  
Db 313 TTACTTCCCTAACCTTCTCTCAGGCTCTCTCCAAAGCGGTGGCTCTTTATTTGGGCCCAT 372  
QY 349 CCAATCTTGATCTCTCACTGTTTATGGTCTCTCGGCCATGAATCGGCCCATCATGCTCTT 408  
Db 373 GCAAGTTGCAATTTTGAACCGGGTTTGGGTATAGCCCATGAATGTGGCCACCATGCTTT 432  
QY 409 TAGTGAGTACCAAGTGAATGAACCGCGTTTGGATTCGTCCTCCATTCGGCTCTCTCTCAC 468  
Db 433 CAGTGATTATCAATGGCTTGACGACAGCGTGGGCTTATCTCTCCACTCTCTCTCTCTAGT 492  
QY 469 CCGTTACTTTCTTGGAAATACAGCCATCGAAGCAAGCAATGCAAAACAAATTCATCGA 528  
Db 493 TCCATATTTCTCTTGGAAATATAGCCACCGCGGTCAACCATTCACACCGGTTCCCTCGA 552  
QY 529 AAACGAGGAAGTTTACATTCCTCCTAGAACTCAGTCCCGAGCTCAGGACTTACTCCACATAGA 588

Db 553 AAGGGATGAAGTGTTCGTTCCCAAGAAAAAATCTGGTTTAAAGTGTGGGCGCAACAC-- 610  
QY 589 ATTTCTTGAACAACAGCGCTGGTTCGAATCCCTCATCTTGGTCATCATGTTAACCTTAGGATT 648  
Db 611 ----TTCAACAATCCACCGGTCGGTTTCTGTCAATCACCATTCAACTTACCTTGGTTG 666  
QY 649 TCCTTTATACCTCTTAACGAATGTTTCAGGCAAGAAGTACGATAGATTTTACCAACCACTT 708  
Db 667 GCCGCTTTACTTAGCTTTCAAGTTGCGGCGCGCTTACGACAGGTTGCTTGGCCACTA 726  
QY 709 TGATCCATTGAGCCCGATCTTTCACGAGCGTGAAGCAATCAGGTTGCTTATCAGATCT 768  
Db 727 TGACCTTTACGGCCCATATTTTCGACCGGGAACGACTCCAAATCTATATCTCTGACGC 786  
QY 769 TGGTATCGTTGCACTGTTTACGACCTCAAGTTTCTTGTAACAAACAAAGGATTTGGTTG 828  
Db 787 CGGCGTCTCGCTCTCGCTATGCGCTCTACCGTCTCGTGTGGCCAAAGGGTGGTTG 846  
QY 829 GGTGATGTGCATGTATGGAGTTCCAGTGTAGTAGGTCTGAATTCCTTTCATTTATCGTAATCAC 888  
Db 847 GGTATTAGCGTTTATGGGTGCGCATTTATGGTGGTTTAAACGCTTCTTAGTAATGATCAC 906  
QY 889 TTATCTGCACCAACACATCTCTGTCACCCCATTTACGATTTCAACCGAATGGAATCGAT 948  
Db 907 GTATTTGCAACACACTCAACCATCTTTGCGCGCACTATGATTTCTCGGAGTGGGACTGGAT 966  
QY 949 CAAAGGAGCTTTGACCAACATTCGACAGAGATTTCCGCTCTCTGAATCGGTTTTCACGA 1008  
Db 967 GAGAGGAGCTTTTATCAACTGTGGACAGAGATTTATGGGATTTTAAACAAAGGTTTTCATPAA 1026  
QY 1009 CGTTTACACACACCCACGCTGTTGCAACCATTTGTTTCCCTTACATTCGACATTTATGCAAA 1068  
Db 1027 CATAAACGACACTCATGTGGCTCATCTATTTGTTTTCGACATGCTCTACTATCATGCCAT 1086  
QY 1069 GGAGGCAAGCGAGCCCATCAAGCCAAATCTTGGGTGATTTACAGGATGATCGACAGACTCC 1128  
Db 1087 GGTGGCCACCAAGCGATAAAGCCATATTTGGGGGAATCTATCATGTTTCGATGGGATGCC 1146  
QY 1129 ATTTTTCAAAGCAATGTGGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGCGA 1188  
Db 1147 TGTCTATAAGCGATATGAGGAGGCGGAAGGAGTGTCTCTACGTTGAACCAAGATGAGGG 1206  
QY 1189 CAGCAAGCACAAAGGACATATTTGTTACCATATAAATGTAATCGATGATGGAGTTT 1243  
Db 1207 CGACAGGATTAAGGTGTGTTTGGTTTAGAACAAGCTTTAAATATTTGCAATT 1261

## RESULT 13

US-10-185-578-1  
; Sequence 1, Application US/10185578  
; Patent No. 6974893  
; GENERAL INFORMATION:  
; APPLICANT: Shanklin, John  
; APPLICANT: White, Edward J.  
; TITLE OF INVENTION: Isoform of Castor Oleate Hydroxylase  
; FILE REFERENCE: DOW-07606  
; CURRENT APPLICATION NUMBER: US/10/185,578  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/302,801  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1164  
; TYPE: DNA  
; ORGANISM: Ricinus communis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1164)  
; OTHER INFORMATION:  
US-10-185-578-1

Query Match 29.7%; Score 417.2; DB 4; Length 1164;

Best Local Similarity 62.1%; Pred. No. 1.1e-104; Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

QY 138 AACGAGCCCGGATTTGATCGGGGCCATCTCGTTAAAGTGTATCTAAAGAAAGCAATCCCTG 197

Db 77 AGGAGCGCGGACACAGAACCTCTTTTACACTTGTGTACCTCAAGAGAGCAATCCAC 136

QY 198 CACATTGCTTCGGCGATCGCGCTCTGCTGTCATCTGCTAGTTCAGGATCTCATTA 257

Db 137 CCATTGCTTTGAACGCTCTTTTGTGGCTCATCTCTCTATGCTATGCTATGCTCTGCT 196

QY 258 TCACCTTCTTTTATACAGGTGCGCAACACCTACATTCCTCACTCCCTCCCTCTAG 317

Db 197 TAAGTTTCTTTTCTACTGATCGCCACCAACTTCTTCCCTTACATCTCTTCTCCGCT 256

QY 318 TTTACTTAGCATCGCGGTTTACTGTTTGGCAATCTTGCACTCTCACTGTTTATGG 377

Db 257 CGTATGCTGCTGCTGTTTACTGCTCTTCCAGGCTGCACTTCACTGCTTGG 316

QY 378 TCCTGGCCATGAATCGGCCATCATGCTCTTATGAGTACCACTGATGATTAACGCCG 437

Db 317 TCATCGCCATGAATGCGCATCATGCTTTTATGAGTATCAGCTGGCTGATGACATTG 376

QY 438 TTGGATTGCTTCCATTTGGCTCTCTCTCACCCCTTACTTTCTTGGAAATACAGCATC 497

Db 377 TTGGCTTAATTTGCTTCTGCACTTCTGCTTCCATATTTTTCATGGAATATAGCCATC 436

QY 498 GAAAGCACCATGCAACACAAATTTCACTCGAAACGAGGAAGTTTACATTTCTTGAATC 557

Db 437 GCGCCACCACTTTAATAGTATGCTCTGAGGAGAGCAAGTGTGCTCCGGAATCAA 496

QY 558 AGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACGCTCTGTCGAATCC 617

Db 497 AGTCGAAATTTTCACTGTTTCTTAAAGTAC-----TTAAACAAACCCGCGAGGTTT 550

QY 618 TCATCTTGTGTCATGTTAACTTAGGATTTCTTTTATACCTCTTAAAGAAATTTTTCAG 677

Db 551 TGACACTTGTGTCAGGCTCTCTTGTGGCTGCTTATATCTTAGCTTTCAATGTCTCTG 610

QY 678 GCAGAAGTACGATAGATTTACCAACCACTTTCATGCTGAGCCGATCTTCCACGAGC 737

Db 611 GTAGACCTTACGATCGCTTGTGCTGCTATGATCCCTATGCGCAATATTTTCCGAA 670

QY 738 GTGAGCGAATCCAGGTTGCGTTATCAGATCTGCTGATCGTTGAGTGTCTTACGACTCA 797

Db 671 GAGAAAGCTTCAGATTAGTTGCTGACCTCGAATCTTGGCAACAGCTTGTGCTTT 730

QY 798 AGTTTCTGTACAAAAGAAAGTGTGTTGGTGATGTCATGATGAGGATTCAGTGA 857

Db 731 ATCAGGCTACAAATGGCAAAAGGTTGGCTTGGGTAATGCTATCTATGGGTCGCAATGC 790

QY 858 TAGGTCGAAATCTTCAATTCGTAATCACTTATCTGCAACACACATCTGCTGCTAC 917

Db 791 TTATGTTAACTGTTTCTTCTTGTATGATCACTACTTTCGAGCACACTCACCAGCTATTC 850

QY 918 CCCATTACGATTCACCGAATGAACTGGATCAAGAGGCTTTGACCAACATCGACAGAG 977

Db 851 CAGCTATGCTCATCGAATGGATTTGGCTCGGGGAGCAATGGTCACTGTCGATAGAG 910

QY 978 ATTTCCGCTCTCTGAAATCGGGTTTTCCACGCTTTACACACCCAGTGTTCGACCAAT 1037

Db 911 ATTATGGGGTGTGAATAAAGTATTCATAAATTCAGACACTCATGTAGCTCATCATC 970

QY 1038 TGTTTCCCTACATTCACATTAATCATGCAAGAGGCGAGCGAGGCAATCAAGCCATCT 1097

Db 971 TCTTTGCTACAGTGCCACATTAATCAATGGAATGGAGGCACTAAGCAATCAAGCCATAA 1030

QY 1098 TGGGTGATTAACAGGATGATCGACAGGACTCATTTTTTCAAGCAATGTGGAGAGAGCCCA 1157

Db 1031 TGGGTGATTAATACCGGTATGATGATACCCATTTTACAAGGCAATGTGGAGGAGGCA 1090

QY 1158 AGGAATGCAATTTACATCGAACAAAGATGACAGACGACCAAGAGGACATATTTGGTACC 1217

Db 1091 AGGAGTGTGTTGTCGAGCCAGATGAAGGAGTCTCTACACAAGCGGTTTCTGGTACC 1150

QY 1218 ATAAATGTAAAT 1229

Db 1151 GGAACAAGTATT 1162

RESULT 14

US-08-314-596-43

; Sequence 43, Application US/08314596

; Patent No. 5668292

; GENERAL INFORMATION:

; APPLICANT: SOMERVILLE, CHRIS

; APPLICANT: VAN DE LOO, FRANK

; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO

; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DABBY & CUSHMAN L.L.P.

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/314,596

; FILING DATE: 26-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: KOKULIS, PAUL N.

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 206905/1220

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1222 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-314-596-43

Query Match 29.7%; Score 417.2; DB 2; Length 1222;

Best Local Similarity 62.1%; Pred. No. 1.2e-104;

Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

QY 138 AACGAGCCCGGATTTGATCGGGGCCATCTCGTTAAAGTGTATCTAAAGAAAGCAATCCCTG 197

Db 37 AGGAGCGCGGACACAGAACCTCTTTTACACTTGTGTACCTCAAGAGAGCAATCCAC 96

QY 198 CACATTGCTTCGGCGATCGCGCTCTGCTGTCATCTGCTAGTTCAGGATCTCATTA 257

Db 97 CCATTGCTTTGAGACGCTCTTTTGTGGCTCATCTCTCTATGTTGCTATGATGCTGCT 156

QY 258 TCACCTTCTCTTTTATACAGGTGCGCAACACCTTCACTCCCTCCCTCTCTAG 317

Db 157 TAAGTTTCTTTTCTACTGATCGCCACCAACTTCTTCCCTTACATCTCTTCCGCTCT 216

QY 318 TTTACTTAGCATCGCGGTTTACTGTTTGGCAATCTTGCATCTCTGTTTATGG 377

Db 217 CGTATGCTGCTGCTGTTTACTGCTCTTCCAGGCTGCACTTCTCACTGCTTTGG 276

QY 378 TCCTCGGCGCATGAATCGCGGCATCATGCTCTTTAGTGAGTACCAAGTGGATTGATAACGCCG 437

Db 277 TCATCGGCCATGAATGCGGCATCATGCTTTTATGAGTATCAGCTGGCTGATGACATTG 336

QY 438 TTGGATTCGTCTCTCAATTCGGCTCTCCTCACCCCTTACTTTCTTGGAAATACAGCCATC 497  
DB 337 TTGGCCTAATTTGCTCAATTCCTGCACTTCTGGTTCCATATTTTTCATGGAAATATAGCCATC 396  
QY 498 GAAAGCACATTCGAAACAAATTCACCTCGAAACGAGAGAGTTTACATCTCTGAACTC 557  
DB 397 GCCGCCACATCTTAACATAGAGTCTCTCGAGGAGAGAGAGTGTCTGTCGGAATCAA 456  
QY 558 AGTCCCACTCAGGACTTACTCCACATACGAATTTCTTGACAACAGCGCTGGTGGAAATCC 617  
DB 457 AGTCGAAATTTCAATGATTTCTAAGTACTCA-----AACACCCGCCAGGTGAGTTT 510  
QY 618 TCATCTTGGTCATCATGTTAACTTACCACTTACCTTTTATACCTCTTAACGAATGTTTCAG 677  
DB 511 TGACACTTGTGTCACCTTCTGCTTGGCTTGGCTTTTATCTTAGCTTTCAATGTCCTG 570  
QY 678 GCAAGAACTACGATAGATTTTACCAACCACTTTTGAATCCATTTAGCCCGGATCTTCCAGCGAGC 737  
DB 571 GTAGACCTTACGATCGCTTGTGCTGCAATATGATCCCTATGGCCCAATATTTCCGAA 630  
QY 738 GTAGCGAATCAAGCTTGGTTATCAGATCTTGGTATCGTTGCACTGTTTACGAGCTCA 797  
DB 631 GAGAAAGGCTTCAGATTTACATTTGCTGACCTCGGAATCTTTGCCACAACGGTTTGTGCTT 690  
QY 798 AGTTCTTGTACAAACAAAGATTTGGTTGGTGATGTCATGATGTCATGATGTCAGTTCAGTGA 857  
DB 691 ATCAGGCTACAAATGCAAAAGGGTTGGCTTGGGTAATGCGTATCTATGGGGTGCCATGTC 750  
QY 858 TAGGTCTGAATTCCTTCAATTCATGTAATCACTTATCTGCACACACACATCTGTGTCAC 917  
DB 751 TTATTTGTAATCTTCTTCTTGTATGATCAGATCTTGCAGCAGACTCACCCAGCTATTC 810  
QY 918 CCCATTACGATTTCAACCGAATGGAATCGAATCAAAAGGAGCGCTTGACCAATTCGACAGAG 977  
DB 811 CACGCTATGGCTCATCGGAATGGGATTTGGCTCCGGGGAGCAATGGTGATGTCGATAGAG 870  
QY 978 ATTTGGTCTCTGATCGGGTTTCCAGGAGTTTACACACACCCAGCTTGTGACCAAT 1037  
DB 871 ATTATGGGGTGTGAATAAGTATTTCCATAATTTGCAGACACTCATGTAGCTCATCATC 930  
QY 1038 TGTTTTCCCTACATTCACATTCATGCAAAAGGAGCGAAGCGAGCCATCAAGCCAAATCT 1097  
DB 931 TCTTTGCTACAGTGCCACATTAACATGCAATGCAATGGAGGCCACTAAGCAATCAAGCCATAA 990  
QY 1098 TGGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATGTGGAGAGGCCA 1157  
DB 991 TGGGTGAGTATTACCGGTATGATGTTACCCCATTTTACAAGGCAATGTGGAGGGAGGCAA 1050  
QY 1158 AGGAATGCAATTTACATCGAGCAAGATGCGACAGCAAGCAACAAAGGACATATTGGTACC 1217  
DB 1051 AGGAGTGTCTTGTCTCGAGCCAGATGAAGGAGCTCTCTACACAAAGGCGGTTTCTGGTACC 1110  
QY 1218 ATAAAAATGTAAT 1229  
DB 1111 GGAACAAGTATT 1122

RESULT 15  
US-08-320-982-43  
Sequence 43, Application US/08320982  
Patent No. 5801026  
GENERAL INFORMATION:  
APPLICANT: SOMERVILLE, CHRIS  
APPLICANT: VAN DE LOO, FRANK  
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABY & CUSHMAN L.L.P.  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,982  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,596  
FILING DATE: 26-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 206905/1220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1222 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-320-982-43

Query Match 29.7%; Score 417.2; DB 2; Length 1222;  
Best Local Similarity 62.1%; Pred. No. 1.2e-104;  
Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;  
QY 138 AACGAGCGCCGATTCGCGGCCATTCCTGTTAAGTGATCTAAAGAAAGCAATCCCTG 197  
DB 37 AGCAGCGCGCACACGAAAGCTCTCTTTCACACTTGGTGACCTCAAGAGAGCCATCCAC 96  
QY 198 CACATTTGCTCGGCGATCCGCGCTGCTGTCATCTGCTAGTAGTTTCAAGATCTCATTA 257  
DB 97 CCCATTTGTTGAACGCTCTTTTGTGGCTCATCTCTCTATGTTGCTGCTCTGCT 156  
QY 258 TCACCTCTCTTTTATACACGGTTCGCAACACACTACATTCCTCACCTCCTCCTCTAG 317  
DB 157 TAAGTTTCTTTTCTACTCGATCGCCACCACTTCTTCCCTTACATCTCTTCTCGCTCT 216  
QY 318 TTTACTTAGCATGCGCGGTTTACTGTTTTCGCAATTTGCAATCTCTCACTGTTTATGG 377  
DB 217 CGTATGCTGCTTGGCTGTTTACTTGGCTCTTCCAAGGCTGCATCTCACTGCTCTTGG 276  
QY 378 TCCTCGGCGCATGAATGCGGCCATCATGCTTTAGTAGTACAGTGGATTGATACGCG 437  
DB 277 TCATCGGCGCATGAATGCGGCCATCATGCTTTTAGTAGTATCAGCTGGCTGATGACATG 336  
QY 438 TTGGATTCGTCTCCATTCGGCTCTCTCTCACCCCTTACTTTTCTGGAAATACAGCCATC 497  
DB 337 TTGGCTAATTTGTCATTTCTGCACTTCTGTTTCCATATTTTTCATGGAAATATAGCCATC 396  
QY 498 GAAAGCACATTCGAAACAAATTCACCTCGAAACGAGAGAGTTTACATTCCTAGAACTC 557  
DB 397 GCCGCCACATTCGAAACATAGGATCTCTCGAGGAGAGAGAGTGTCTGTCGGAATCAA 456  
QY 558 AGTCCCACTCAGGACTTACTCCACATACGAATTTCTTGACAACAGCGCTGGTGGAAATCC 617  
DB 457 AGTCGAAATTTCAATGATTTCTAAGTACTCA-----AACACCCGCCAGGTGAGTTT 510  
QY 618 TCATCTTGGTCATCATGTTAACTTACCACTTACCTTTTATACCTCTTAACGAATGTTTCAG 677  
DB 511 TGACACTTGTGTCACCTTCTGCTTGGCTTGGCTTTTATCTTAGCTTTCAATGTCCTG 570  
QY 678 GCAAGAACTACGATAGATTTTACCAACCACTTTTGAATCCATTTAGCCCGGATCTTCCAGCGAGC 737  
DB 571 GTAGACCTTACGATGCTGTTTGGCTTGGCTTATGATCCCTATGGCCCAATATTTCCGAA 630

Qy	738	GTGAGCGAATCCAGGTTCGGTTATCAGATCTTGGTATCGTTGCGAGTGTTCACGGACTCA	797
Db	631	GAGAAAGGCTTCAGATTACATTGCTGACCTCGGAATCTTTGCCACAACGTTTGTGCTTT	690
Qy	798	AGTTTCTTGTACAAACAAAGGATTTGGTTGGTGATGTGCATGTATGGAGTTCAGTGA	857
Db	691	ATCAGGCTACATGGCAAAAGGTTGGCTTGGTAATGCGTATCTATGGGGTGCCATTGC	750
Qy	858	TAGGTCTGAATTCCTTCATTATCTGTAATCACATTATCTGCACCACACACATCTGTCTGCAC	917
Db	751	TTATTGTTAACTGTTTCCTTGTATGATCACATACCTTGCAGCACACTCACCCAGCTATTTC	810
Qy	918	CCCAITACGATTCAACCGAATGGAACTGGATCAAGAGCCTTGGACCAACAATCGACAGAG	977
Db	811	CACGCTATGGCTCATCGGAATGGGATTTGGCTCCGGGGAGCAATGGTCACTGTGATAGAG	870
Qy	978	ATTTCGGTCTCCTGAATCGGTTTTCACGACGTTACACACACCCACGTTGTCACCATTT	1037
Db	871	ATTATGGGGTGTGAATAAGTATTCATAACATTCGACACACTCATGTAGCTCATCATC	930
Qy	1038	TGTTTCCCTACATTCACACATTATCGCAAGGAGGCAAGCGAGGCCATCAAGCCAACTCT	1097
Db	931	TCCTTCTACAGTCCACATTTACCATGCAATGGAGGCCACTAAGCAATCAAGCCTATAA	990
Qy	1098	TGGTCAATTACAGGATGATCGACAGACTCCCATTTTCAAAGCAATGTGGAGAGAGGCCA	1157
Db	991	TGGGTGAGTATTACCGGTATGATGGTACCCCAATTTTACAAGGCATTGTGGAGGGAGCAA	1050
Qy	1158	AGGAATGCCATTTACATCGAGCAGATGCGACAGACGACCAAGCACAAGGGACATATTGGTACC	1217
Db	1051	AGGAGTGTCTTGTCTCGAGCCAGATGAAGGAGCTCCTACACAAGGCGTTTCTGTGTACC	1110
Qy	1218	ATAAAATGTAAT	1229
Db	1111	GGNACAAGTATT	1122

Search completed: September 25, 2006, 01:08:35  
Job time : 298 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2006, 22:33:01; Search time 1361 Seconds  
(without alignments)  
7202.778 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
Sequence: 1 gtaggtttgggtgcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1406	100.0	1406	14	Adw68586 Stokesia
2	870	61.9	1364	2	Aav72550 Vernonia
3	870	61.9	1364	14	Adw68594
4	697	49.6	1137	14	Aec02364 Stokesia
5	681.6	48.5	1134	13	Adr87346 Hydroxyyla
6	681.6	48.5	1134	14	Aec02260 Stokesia
7	673	47.9	1285	4	Aaf88311 C. offic
8	665.6	47.3	1134	13	Adr87352 Codon opt
9	665.6	47.3	1134	14	Aec02266 Stokesia
10	657.8	46.8	1125	13	Adr87325 Hydroxyyla
11	657.8	46.8	1125	14	Aec02239 Crepis bi
12	657.6	46.8	1312	2	Aav63102
13	646	45.9	1143	13	Adr87331 FAD2/Hydr
14	646	45.9	1143	14	Aec02245
15	640.4	45.5	1344	14	Adw68595
16	640.4	45.5	1358	2	Aav63101
17	640.4	45.5	1358	14	Adx69238 Delta-12
18	640.4	45.5	1358	14	Adx85617 DNA encod

19	640.4	45.5	1358	14	Adw88813
20	638.6	45.4	1125	13	Adr87351
21	638.6	45.4	1125	14	Aec02265
22	612.8	43.6	1435	14	Adx18009
23	612.8	43.6	1435	14	Adx69236
24	612.8	43.6	1435	14	Adx85615
25	611.2	43.5	1128	2	AAT95688
26	486.4	34.6	1134	13	Adr87348
27	486.4	34.6	1134	14	Aec02262
28	470.6	33.5	1125	14	Aec02365
29	467.2	33.2	1125	14	Aec02363
30	467	33.2	6220	12	Adh51189
31	467	33.2	6220	12	ADI03850
32	462.6	32.9	1586	13	Adx31958
33	459.8	32.7	1457	13	Adx29962
34	440.4	31.3	1640	10	Adf55608
35	430.6	30.6	1152	13	Adr87326
36	430.6	30.6	1152	14	Aec02240
37	430.6	30.6	1541	13	Adr60394
38	426.2	30.3	1369	6	AbL58599
39	426.2	30.3	1372	2	AAQ66068
40	426.2	30.3	1372	3	AAZ51315
41	426.2	30.3	1372	14	ADY79693
42	426.2	30.3	1615	14	AEb48230
43	426.2	30.3	1619	13	Adr89457
44	424.6	30.2	1451	3	AAc39493
45	424.6	30.2	2973	2	AAQ66074

ALIGNMENTS

RESULT 1

ADW68586

ID ADW68586 standard; cDNA; 1406 BP.

XX AC ADW68586;

XX DT 07-APR-2005 (first entry)

XX DE Stokesia laevis fatty acid epoxigenase cDNA.

XX KW DNA purification; transgenic plant; plant; expression; recombinant DNA;

XX KW seed oil; soybean oil; linseed oil; plastic;

XX KW delta 12-fatty acid epoxigenase; delta 12-epoxigenase;

XX KW delta 12-epoxidase; gene; ds; transgene.

XX OS Stokesia laevis.

XX FH Key Location/Qualifiers

XX FT CDS 92..1228

XX FT /\*tag= a

XX FT /product= "Stokesia laevis fatty acid epoxigenase"

XX PN US2005022270-A1.

XX PD 27-JAN-2005.

XX PF 21-JUL-2003; 2003US-00622774.

XX PR 21-JUL-2003; 2003US-00622774.

XX PA (HILD/) HILDEBRAND D.

XX PA (HATA/) HATANAKA T.

XX PI Hildebrand D, Hatanaka T;

XX DR WPI; 2005-111979/12.

XX DR P-PSDB; ADW68587.

XX PT New isolated nucleic acid molecule encoding a delta 12-fatty acid epoxigenase enzyme, useful for genetically producing industrial products including coating, composites, adhesives and plasticizers.



XX PS Claim 5; SEQ ID NO 1; 22pp; English.

CC The present invention relates to a nucleic acid molecule encoding a delta

CC 12-fatty acid epoxigenase enzyme. The invention is useful for genetically

CC producing raw materials in the manufacture of industrial products

CC including coating, composites, adhesives and plasticizers. The present

CC sequence is the Stokesia laevis fatty acid epoxigenase cDNA.

XX SQ Sequence 1406 BP; 403 A; 322 C; 289 G; 392 T; 0 U; 0 Other;

Query Match 100.0%; Score 1406; DB 14; Length 1406;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGGTTTGGGTCGGTGAGATCAGTGTTCGACCGAAATCCAAACGCAATTTCTAAATTT 60

Db 1 GTAGGTTTGGGTCGGTGAGATCAGTGTTCGACCGAAATCCAAACGCAATTTCTAAATTT 60

Qy 61 GGATTTGAAATCTGGGAGAGGTAGCAGATGTCCGATTCATATGATGATCGAATGAA 120

Db 61 GGATTTGAAATCTGGGAGAGGTAGCAGATGTCCGATTCATATGATGATCGAATGAA 120

Qy 121 AGATCATGATATGACGACGAGCCCGATTTGATTCGGCGCATCTCTGTTAAGTGATCT 180

Db 121 AGATCATGATATGACGACGAGCCCGATTTGATTCGGCGCATCTCTGTTAAGTGATCT 180

Qy 181 AAGAAAGCAATCCCTGCACATTTGTTCCGGCGATTCGGCGCATCTCTGTTAAGTGATCT 240

Db 181 AAGAAAGCAATCCCTGCACATTTGTTCCGGCGATTCGGCGCATCTCTGTTAAGTGATCT 240

Qy 241 AGTTCAGATCTCATATATCAGTCTCTTTTATACAGGTTCGCAACCTCATCTCTCA 300

Db 241 AGTTCAGATCTCATATATCAGTCTCTTTTATACAGGTTCGCAACCTCATCTCTCA 300

Qy 301 CCTCCTCCTCCTAGTCTTACTAGCATGCGCGTTTACTGTTTTCGCCAATCTTGAT 360

Db 301 CCTCCTCCTCCTAGTCTTACTAGCATGCGCGTTTACTGTTTTCGCCAATCTTGAT 360

Qy 361 CCTCAGTGGTTTATGGTCTCTCGGCATGAATGCGGCATCATGCTTTAGTGATACCA 420

Db 361 CCTCAGTGGTTTATGGTCTCTCGGCATGAATGCGGCATCATGCTTTAGTGATACCA 420

Qy 421 GTGATTTGATTAACGCGTTGATTTGCTCCTCATTTGCGCTCTCTCACCCTTACTTTTC 480

Db 421 GTGATTTGATTAACGCGTTGATTTGCTCCTCATTTGCGCTCTCTCACCCTTACTTTTC 480

Qy 481 TTGGAATACAGCCATCGAAAGCACCATGCAAAACAAATTCACCTCGAAACGAGGAAT 540

Db 481 TTGGAATACAGCCATCGAAAGCACCATGCAAAACAAATTCACCTCGAAACGAGGAAT 540

Qy 541 TTACATTCCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACGAATTTCTTGCAA 600

Db 541 TTACATTCCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACGAATTTCTTGCAA 600

Qy 601 CACGCTGGTGAATCTCATCTTGGTCACTATGTTTAACTTACCTAGGATTTCTTTATACCT 660

Db 601 CACGCTGGTGAATCTCATCTTGGTCACTATGTTTAACTTACCTAGGATTTCTTTATACCT 660

Qy 661 CTTTACGAATGTTTTCAGGCAAGAAGTACGATGATTTTACCAACCTTTTGATTCATTCGAG 720

Db 661 CTTTACGAATGTTTTCAGGCAAGAAGTACGATGATTTTACCAACCTTTTGATTCATTCGAG 720

Qy 721 CCCGATCTTCCAGGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC 780

Db 721 CCCGATCTTCCAGGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC 780

Qy 781 AGTGTGTTTACGACTCAAGTTCTTGTACAAACAAAGGATTTGGTGGTGGTGGTGGAT 840

Db 781 AGTGTGTTTACGACTCAAGTTCTTGTACAAACAAAGGATTTGGTGGTGGTGGTGGAT 840

Qy 841 GTATCGAGTTCCAGTGATAGGTTCTGAATTCCTTCAATTCGTAATCTATCTGACCA 900

Db 841 GTATCGAGTTCCAGTGATAGGTTCTGAATTCCTTCAATTCGTAATCTATCTGACCA 900

Db 841 GTATCGAGTTCCAGTGATAGGTTCTGAATTCCTTCAATTCGTAATCTATCTGACCA 900

Qy 901 CACACATCTGCTGCTACCCCATTTACGATTTCAACCGAATGGAATCGATCAAGAGGCTT 960

Db 901 CACACATCTGCTGCTACCCCATTTACGATTTCAACCGAATGGAATCGATCAAGAGGCTT 960

Qy 961 GACCAATTCGACAGAGATTTCCGTCCTCCGATTCGAGTTCGAGTTCACGACCTTACACAC 1020

Db 961 GACCAATTCGACAGAGATTTCCGTCCTCCGATTCGAGTTCGAGTTCACGACCTTACACAC 1020

Qy 1021 CCAGCTGTTGCACCATTTTGTTCCTACATTCACATTCATCATGCAAGGAGCAAGCGA 1080

Db 1021 CCAGCTGTTGCACCATTTTGTTCCTACATTCACATTCATCATGCAAGGAGCAAGCGA 1080

Qy 1081 GGCCATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGC 1140

Db 1081 GGCCATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGC 1140

Qy 1141 AATGTGGAGAGAGCCCAAGGAATGCAATTTACATCGAGCAAGATGACACAGCAAGCAAA 1200

Db 1141 AATGTGGAGAGAGCCCAAGGAATGCAATTTACATCGAGCAAGATGACACAGCAAGCAAA 1200

Qy 1201 AGGACATATTTGGTACCATTAATAATGTAATCGATGAGTGTAGTTTGGAAATAATGACA 1260

Db 1201 AGGACATATTTGGTACCATTAATAATGTAATCGATGAGTGTAGTTTGGAAATAATGACA 1260

Qy 1261 TGCAGCATCTCTTGTATGCTTGAATCGTTCATTTCTTTATATGTTTGTAAAGATAAA 1320

Db 1261 TGCAGCATCTCTTGTATGCTTGAATCGTTCATTTCTTTATATGTTTGTAAAGATAAA 1320

Qy 1321 TAAGTAATCTTTGAGTGAAGATGGGAGCAGGAACAAAGCAAGATAATAATACGCTAAAA 1380

Db 1321 TAAGTAATCTTTGAGTGAAGATGGGAGCAGGAACAAAGCAAGATAATAATACGCTAAAA 1380

Qy 1381 AAAAAAAAAAAAAAAAAAAAAA 1406

Db 1381 AAAAAAAAAAAAAAAAAAAAAA 1406

RESULT 2

AAV72550

ID AAV72550 standard; cDNA; 1364 BP.

XX AC AAV72550;

XX DT 27-AUG-2003 (revised)

DT 10-FEB-1999 (first entry)

XX XX Vernonia galamenensis fatty acid epoxidising enzyme encoding cDNA.

XX XX Vernonia galamenensis; fatty acid desaturase; epoxidising enzyme;

KW expression; chimeric gene; recombinant enzyme; ss.

XX OS Vernonia galamenensis.

PH Key Location/Qualifiers

FT CDS 103..1257

FT /\*tag= a

XX US5846784-A.

XX PN 08-DEC-1998.

PD 11-JUN-1997; 97US-00872302.

PF 11-JUN-1997; 97US-00872302.

PR 11-JUN-1997; 97US-00872302.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

PA Hitz WD;

XX WPI; 1999-059065/05.

DR P-PSDB; AAW83354.

XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid  
PT epoxidising enzyme - used to alter levels of expression of the enzymes in  
PT transformed host cells or to produce recombinant enzymes.

XX Claim 6; Col 25-29; 21pp; English.

XX The present sequence encodes Vernonia galamensis fatty acid epoxidising  
CC enzyme. The present invention also describes: (i) Vernonia galamensis  
CC fatty acid desaturase; (ii) chimeric genes comprising the fragments  
CC linked to regulatory sequences; and (iii) transformed host cells  
CC containing the chimeric genes. The DNA's from the present invention can  
CC be used to alter levels of expression of the enzymes in transformed host  
CC cells or to produce the recombinant enzymes by transformation of  
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;

Query Match 61.9%; Score 870; DB 2; Length 1364;  
Best Local Similarity 86.1%; Pred. No. 5.9e-206;  
Matches 963; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY	120	AGATCATCATATGAGCAACGACCGCCGATTCGATCGCGCCATTCCTCGTTAAGTGATC	179
DB	149	ATGATCATTAATAACGAACGTGCACCGGTGATCGCGACCAATTCCTGTTAAGCGATC	208
QY	180	TAAAGAAACAAATCCCTGCACATTCGCTCCGCGATCCGCGCTCTGGTTCATCTCTGCTACG	239
DB	209	TAAAGAAACAAATCCCTCGCATTCGCTCCGCGATTCGCTCCGCGATTCGCTGCTACG	268
QY	240	TAGTTGAGATCTCATATATACCTTCCTTTTATACAGGTGCGCAACACTACATTCCTC	299
DB	269	TGTTTCAGGATCTCATATATATACCTTCCTTTTATACAGGTGCGCAACACTACATTCCTC	328
QY	300	ACCTCCCTCCTCTAGTTTACTAGCATGCGCGTTCCTGCTGCTGCTGCTGCTGCTGCTG	359
DB	329	TTCTTCCTCCTCTACCTTACTTATAGCATGCGCGTTCCTGCTGCTGCTGCTGCTGCTG	388
QY	360	TCCTCACTGTTTATGGGTCCTCGGCATGAAATCGCGCCATCATGCTTTAGTGATGAC	419
DB	389	TCCTCACTGTTTATGGGTCCTCGGCATGAAATCGCGCCATCATGCTTTAGTGATGAC	448
QY	420	AGTGAATGATTAACGCGCTTGATTCGCTCCTCATTCGCGCTCTCTCAACCCCTTACTTT	479
DB	449	AGTGGGTTGATAACACCGTTGGATTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	508
QY	480	CTTGGAAATACAGCCATCGAAAGCACCATGCAACAAATTCACCTCGAAACAGGAG	539
DB	509	CTTGGAAATACAGCCATCGAAAGCACCATGCAACAAATTCACCTCGAAACAGGAG	568
QY	540	TTTACATTCCTAGAACTCAGTCCAGCTCAGGCTTACTCCACATACGAATTTCTTGACA	599
DB	569	TTTACATTCCTAGAACTCAGTCCAGCTCAGGCTTACTCCACATACGAATTTCTTGACA	628
QY	600	ACACGCTGGTTCGAATTCCTCATCTTGGTTCATCATGTTAACTTAGGATTCCTTTATACC	659
DB	629	ACACGCTGGTTCGAATTCCTCATCTTGGTTCATCATGTTAACTTAGGATTCCTTTATACC	688
QY	660	TCTTAACGAATGTTTCAGGCAAGATGATAGATTACCAACCACTTTGATCCATGGA	719
DB	689	TCTTGACCAATATTTTCAGGCAAGATGATAGATTACCAACCACTTTGATCCATGGA	748
QY	720	GCCGATCTTCACGAGGTGAGCAATCCAGTTCGGTTATCAGATCTTGGTATCTGTTG	779
DB	749	GCCGATCTTCACGAGGTGAGCAATCCAGTTCGGTTATCAGATCTTGGTATCTGTTG	808
QY	780	CAGTGTTCAGGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTGGGTGATGCA	839
DB	809	CTGTGTTCAGGCTTAAAGTTTCTTGTAGCGAAGAAAGGTTGGTGGGTGATGCA	868
QY	840	TGTATGGAGTTCAGTGTAGTCTGAATTCCTTCAATATCGTAATCATCTATCTGCACC	899
DB	869	TGTACGGAGCCGAGTGTGGGCTGAATGCGCTTCATAATAATGATCACTTATCTCCACC	928

QY	900	ACACACATCTGTGTGTCACCCCATTTACGATTAACCGAATGGAATCGGATCAAAAGGAGCT	959
DB	929	ACACCCATCTGTGTCCTCGCTCATTTACGATTAACCGAATGGAATCGGATCAAAAGGAGCT	988
QY	960	TGACCAATCGACAGAGATTTCCGCTCTCCTGAATCGGGTTTCCACGACGTTACACACA	1019
DB	989	TGACCAATCGACAGAGATTTCCGCTCTCCTGAATCGGGTTTCCACGACGTTACACACA	1048
QY	1020	CCCAGCTGTGCAACCATTTGTTTCCCTACATTCACATTCATCATGCAAGGAGGCAAGCG	1079
DB	1049	CACACGCTGTGATCATTTGTTTCCCTACATTCACATTCATCATGCAAGGAGGCAAGCG	1108
QY	1080	AGCCCATCAAGCAATCTTGGTGTATACAGATGATGACAGGATCTCATTTTCAAAAG	1139
DB	1109	AGCCCATCAAGCAATCTTGGTGTATACAGATGATGACAGGATCTCATTTTCAAAAG	1168
QY	1140	CAATGTGGAGAGCGCCCAAGGATTCATTTACATCGAGCAAGATCGACAGCAAGCACA	1199
DB	1169	CAATGTGGAGAGCGCCCAAGGATTCATTTACATCGAGCAAGATCGACAGCAAGCACA	1228
QY	1200	AAGGACATATTTGGTACCATTAATAATGTAATCGATGATG	1237
DB	1229	AAGGACATATTTGGTACCATTAATAATGTAATCGATGATG	1266

RESULT 3  
ADM68594  
ID ADM68594 standard; DNA; 1364 BP.  
XX  
AC ADM68594;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Vernonia galamensis epoxigenase cDNA.  
XX  
KW DNA purification; transgenic plant; plant; expression; recombinant DNA;  
KW seed oil; soybean oil; linseed oil; plastic;  
KW delta 12-fatty acid epoxigenase; delta 12-epoxigenase;  
KW delta 12-epoxidase; ds.  
XX  
OS Vernonia galamensis.  
XX  
PN US2005022270-A1.  
XX  
PD 27-JAN-2005.  
XX  
PF 21-JUL-2003; 2003US-00622774.  
XX  
PR 21-JUL-2003; 2003US-00622774.  
XX  
PA (HILD/) HILDEBRAND D.  
PA (HATA/) HATANAKA T.  
XX  
PI Hildebrand D, Hatanaka T;  
XX  
DR WPI; 2005-111979/12.  
XX  
PT New isolated nucleic acid molecule encoding a delta 12-fatty acid  
PT epoxigenase enzyme, useful for genetically producing industrial products  
PT including coating, composites, adhesives and plasticizers.  
XX  
PS Example 4; SEQ ID NO 9; 22pp; English.  
XX  
CC The present invention relates to a nucleic acid molecule encoding a delta  
CC 12-fatty acid epoxigenase enzyme. The invention is useful for genetically  
CC producing raw materials in the manufacture of industrial products  
CC including coating, composites, adhesives and plasticizers. The present  
CC sequence is the Vernonia galamensis epoxigenase cDNA. Note: The present  
CC sequence is described as SEQ ID NO:9 in the sequence listing. But SEQ ID  
CC NO:11 on the page 2 of the specification.  
XX  
SQ Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;

Query Match		61.9%;	Score 870;	DB 14;	Length 1364;
Best Local Similarity		86.1%;	Pred. No. 5.9e-206;		
Matches 963;		Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
Qy	120	AAGATCATGATATGACCAAGAGCCCGATTTGATCCGGCGCCATCTCTCGTTAAAGTGATC	179		
Db	149	ATGATCATATATAAACAAAGTGACCGGTGTGTCGGCCACCATCTCTGTTAAGCGATC	208		
Qy	180	TAAAGAAAGCAATCCCTGCACATTTCTTCGGCGATCCGGCGTCTGTGTCATCCTGCTACG	239		
Db	209	TAAAGAAAGCAATCCCTCGCATTTCTTCAGAGATCTGCCATCGTTTCATCGTCTACG	268		
Qy	240	TAGTTCAGGATCTCATATACCTTCCTTTTATACACGGTCGCCAACACCTACATCTCTC	299		
Db	269	TGTTCAGGATCTCATATACCTTCCTTTTATACACGGTCGCCAACACCTCTTACATCTCTC	328		
Qy	300	ACCTCCCTCCTCTAGTCTTACTTAGCATGGCGGTTTACTGGTTTGGCAATCTTGCA	359		
Db	339	TTCTTCCTCCTCTACTTACTTAGCATGGCCTGTCTTACTGGTTTGGCAATCTTGCA	388		
Qy	360	TCCTCAGTGGTTATGGGTCTCTCGGCCATGAATGGCGCATCATCGCTTTAGTGAGTACC	419		
Db	389	TCCTCAGTGGTTATGGGTCTCTCGGCCATGAATGGCGCATCATCGCTTTAGTGAGTACC	448		
Qy	420	AGTGAATGATAACGCCGTTGGATTCGTCTCCATTCGGCTCTCTCCACCCCTTACTTTT	479		
Db	449	AGTGGGTTGATAAACACCGTTGGATTCATCTCTCCATTCCTTCTTCTCACACCTTACTTTT	508		
Qy	480	CTTGGAAATACGCCATCGAAGACCAATGCAACACAAATTCATCTCGAAGACGGAG	539		
Db	509	CTTGGAAATACGCCATCGAAGACCAATGCAACACAAATTCATCTCGAAGACGGAGG	568		
Qy	540	TTTACATTCCTAGAACTCAGTCCCACTCAGGACTTACTCCACATACGAATTTCTTGACA	599		
Db	569	TTTACATTCCTAAGCCCAAGTCCCACTCAGGAAATTTCTTCAATTTCTTGACA	628		
Qy	600	ACAGCCCTGGTGAATCTCTATTTGGTTCATCATGTTAACTTAACTTCTTTTATACC	659		
Db	629	ACAGCCCTGGTGAATCTCTATTTGGTTCATCATGTTAACTTAACTTCTTTTATACC	688		
Qy	660	TCTTAAACAAATTTTCAGGCAAGATAGATAGATTTACCAACCACTTTCATCATTTGA	719		
Db	689	TCTTAAACAAATTTTCAGGCAAGATAGATAGATTTACCAACCACTTTCATCATTTGA	748		
Qy	720	GCCGATCTTACCGAGCGTGAGCGAATCCAGGTTCGTTATCAGATCTTGTATCGTTG	779		
Db	749	GCCGATCTTACCGAGCGTGAGCGAATCCAGGTTCGTTATCAGATCTTGTATCGTTG	808		
Qy	780	CAGTGTTCACGACTCAAGTTTCTTTGTACAAACAAAGGATTTGGTTGGGTGATGTGCA	839		
Db	809	CTGTGTTCACGACTCAAGTTTCTTTGTAGCAAAAGGGTTCGGTTGGGTGATGTGCA	868		
Qy	840	TGTATGGAGTTCAGTGATAGTCTGAATTCCTTCAATTCGTATCACTTATCTGCACC	899		
Db	869	TGTATGGAGTTCAGTGATAGTCTGAATTCCTTCAATTCGTATCACTTATCTGCACC	928		
Qy	900	ACACATCTGTGCTGCACCCATTAAGTTCACCGAATGGAATCGGATCAAGAGGCT	959		
Db	929	ACACCATCTGTCTGCCTCATTAAGTTCACCGAATGGAATCGGATCAAGAGGCT	988		
Qy	960	TGACCAATACAGAGATTTTCGTCTCTGTAATCGGGTTTTCACGAGTTACACACA	1019		
Db	989	TGACTACAATCATAGAGATTTTCGTCTCTGTAATCGGGTTTTCACGAGTTACACACA	1048		
Qy	1020	CCCAGTGTGACCAATTTGTTTCCCTACATTCACATTCATCATCAAGAGGCAAGG	1079		
Db	1049	CACAGTGTGACCAATTTGTTTCCCTACATTCACATTCATCATCAAGAGGCAAGG	1108		
Qy	1080	AGGCCATCAAGCAATCTTGGGTGATTCAGAGATGATCGACAGGACTCATTTTTCAAAG	1139		
Db	1109	AGCCAAATCAAGCCGTTAGGGAGTATCGAGATGATCGAGTATCGTTTTCACAAAG	1168		
Qy	1140	CAATGTGGAGAGGCCCAAGAAATGCAATTTTACATCGAGCAAGATCGACAGCAAGCACA	1199		
Db	1169	CAATGTGGAGAGGCCCAAGAAATGCAATTTTACATCGAGCAAGATCGAGCAAGCAAGCACA	1228		
Qy	1200	AAGGCACATATTGTGTACCATAAATGTAATCGATGATG	1237		
Db	1229	AAGGTGTATTGTGTACCATAAATGTAATCGATGATG	1266		
RESULT 4					
AEC02364					
ID	AEC02364	standard; cDNA; 1137 BP.			
XX	AEC02364;				
AC	AEC02364;				
DT	06-OCT-2005	(first entry)			
XX	Stokesia laevis	epoxygenase encoding cDNA SEQ ID NO:131.			
DE	transgenic plant;	anthelmintic; epoxygenase; gene; ss.			
XX	Stokesia laevis.				
OS	Key	Location/Qualifiers			
XX	CDS	1..1137			
EH		/*tag= a			
FT		/product= "epoxygenase"			
XX	US2005172358-A1.				
PN	04-AUG-2005.				
XX	04-AUG-2004;	2004US-00912534.			
XX	04-FEB-2004;	2004US-00772227.			
XX	(VERB/) VERBSKY M L.				
PA	(BAUB/) BAUBLITE C.				
PA	(KLOE/) KLOEK A P.				
PA	(DAVI/) DAVILA-APONTE J A.				
PA	(HRES/) HRESKO M C.				
PA	(MCLA/) MCLAIRD M B.				
PA	(ZENT/) ZENTELLA R.				
PA	(WILL/) WILLIAMS D J.				
XX	Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;				
PI	Mclaird MB, Zentella R, Williams DJ;				
XX	WPI; 2005-603337/62.				
DR	P-PSDB; AEC02369.				
XX	New transgenic plant having a DNA construct comprising a nucleic acid				
PT	encoding a protein for catalyzing the conversion of a substrate to a C16,				
PT	C18 or C20 monounsaturated fatty acid product, useful in preparing				
PT	anthelmintic compounds.				
XX	Claim 74; SEQ ID NO 131; 130pp; English.				
PS	The invention relates to a transgenic plant containing at least one DNA				
XX	construct comprising: (a) a nucleic acid encoding a polypeptide effective				
CC	for catalyzing the conversion of a substrate to a C16, C18, or C20				
CC	monounsaturated fatty acid product; and (b) a regulatory element operably				
CC	linked to the nucleic acid encoding the polypeptide and conferring				
CC	expression in a vegetative tissue of the plant. Also described: (1) a				
CC	method of making a transgenic plant; (2) an isolated nucleic acid				
CC	comprising the nucleotide sequence; (3) a recombinant nucleic acid				
CC	construct comprising at least one regulatory element that confers				
CC	expression in a vegetative tissue of a plant; and (4) a method of				
CC	screening a transgenic plant for anthelmintic activity. The transgenic				
CC	plant is useful in preparing compounds having anthelmintic activity. The				
CC	present sequence encodes an epoxygenase which is used in the				
CC	exemplification of the present invention.				

[illegible]



CC exemplification of the present invention.

XX	Sequence	1134 BP; 297 A; 268 C; 229 G; 340 T; 0 U; 0 Other;	
XX	Query Match	48.5%; Score 681.6; DB 14; Length 1134;	
XX	Best Local Similarity	78.0%; Pred. No. 3.9e-159;	
XX	Matches	835; Conservative 0; Mismatches 229; Indels 6; Gaps 1;	
QY	159	CGCCATCTTCGTTAAGTGATCTAAAGAAAGCAATCCCTGCACATTCGTTCCCGCGATCCG	218
DB	71	CACCTTTCACATTAAGTGATATAAAGAAAGCAATCCCTCCCATTCGTTCAACAGATCTG	130
QY	219	CGCTCTGGTCATCCTCGTAGTTCAGATCTCAATATFACCTTCCTTTTATACACGG	278
DB	131	TCATACGTTTCGTCCTACTATGTGTTTCATGATCTCATCGTCTCTACGCTCTCTTCTTC	190
QY	279	TGCGCAACCTACATCTCTCACTCCCTCTCTCTAGTTTACTTAGCATGCGCGTTT	338
DB	191	TGCAACGACATATATTTACTGTTCTTCTGCTCTCTCTGCTTACATAGCGTGCCAGTTT	250
QY	339	ACTGGTTTGGCCAACTCTGCATCCTCACTGGTTTATGGGTCCTCGGCCATGAATCGCGC	398
DB	251	ACTGGTTTGGCCAACTATCTCACTGGGTTGTTGGGTTATCGGCCATGAATGTGTC	310
QY	399	ATCATGCCCTTATGATGATACAGTGAATGATTAACCGCGTTGGAATTCGTCCTCATTCGG	458
DB	311	ACCATGCCCTTATGATGAATACAGTGAATGATGACACAGTTGGGTTTCATCTCCACTCG	370
QY	459	CTCTCCTCACCCCTTACTTTCTTGGAAATACAGCCATCGAAGCACCATGCAACACAA	518
DB	371	CTCTCCTCACCCCTTACTTCTTGGAAATATAGCCATCGAATCACCATGCGAACACAA	430
QY	519	ATTCACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCAGCTCAGGACTTACT	578
DB	431	ATTCACTCGAACAGCAGAGTTTACATTCCTAAGCGCAAGTCCAAGTCAAGTTTACT	490
QY	579	CCACATACGAATTTCTTTGACAAACACCGCTGGTCCGAATCCTCACTCTTGGTCATCATGTTAA	638
DB	491	CCA-----AATCCTTAACCAACCCACCTGGACGAGTGTTCACCTTGGTTTTCAGGTGA	544
QY	639	CCTTAGGATTTCTTTATACCTCTTAACGAATGTTTCAGGCAAGAGTAGATAGATTTA	698
DB	545	CGTAGGGTTTCTTTGTACTCTTCTAGCTGTAATCTACGCAATCAAGCTTCTTGTGTCGAAAG	704
QY	699	CAACACATTTGATTCATGAGCCGATCTTACCGAGGTGAGCAATCCAGTTGCGT	758
DB	605	CAACACATTTGATTCATGAGTCCCATCTTACCAGGCGTGAACGAATTCAGTTCTTG	664
QY	759	TATCAGATCTTGATCGTTGTCAGTGTTTTACGGAATCAAGTTTCTTGACAAACAAAG	818
DB	665	TATCAGATCTTGCTCTTCTAGCTGTAATCTACGCAATCAAGCTTCTTGTGTCGAAAG	724
QY	819	GATTTGGTGGTGATGTCATGTATGGATTTCCAGTATAGTCTGAAATTCCTTCATTA	878
DB	725	GAGCTGTCTGGGTGACATGATCTATGGAGTTCCAGTCTTAGTGTAAGCGTGTCTTCG	784
QY	879	TGCTATCACTTATCTGCAACACACATCTGTCGTACCCCATTAAGATTCAACCGAAT	938
DB	785	TTTTGATACGATTTTACACCAACCCATCTCTCTTACTCTATTAGATTTCAGCTGAGT	844
QY	939	GGAACTGGATCAAGGAGCCTTGACCACAAATCGACAGAGATTTTCGGTCTCCTGAATCGGG	998
DB	845	GGAACTGGATCAGAGGGCATTGTCACCAATCGATAGGATTTTGGGTTCTTAATAGG	904
QY	999	TTTTCCAGCGATTACACACACCGTGTGTGACCAATTTGTTCCCTTACATTTCCACAT	1058
DB	905	TTTTCCATGACGTTTACACACATCTATGTATTGTCATCTTTGATCTTACATTTCCACAT	964
QY	1059	ATCATCAAGGAGGCAAGCGGCCATCAAGCCATCTTGGGTGATTACAGGATCATCG	1118
DB	965	ATCATCAAGGAGGCAAGGATGCAATCAACAGTTTGGGTGATTATTATAAGATTG	1024
QY	1119	ACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGGCAAGGAATGCATTTTACATCGAGC	1178

DB	1025	ATAGGACTCCGATATTTCAAAGCAATGTGGAGAGAGCCCAAGGATGCATCTATATCGAGC	1084
QY	1179	AAGATTGCACAGCAGCAAGCAAAAGGACATATTGGTACCATAAAATGTAA	1228
DB	1085	CAGATGAAGATACTGAACACAAGGGTGTCTTACTGTGTACCATTAATGTGA	1134
RESULT 7			
ID	AAF88311	standard; DNA; 1285 BP.	
XX	AAF88311;		
AC	AAF88311;		
DT	22-AUG-2001	(first entry)	
XX	C. officinalis	calendulic acid desaturase encoding DNA.	
DE	Calendula;	calendulic acid desaturase; unsaturated fatty acid; oil;	
XX	triglyceride; transgenic plant; ds.		
KW	Calendula officinalis.		
OS			
XX	Key	Location/Qualifiers	
PH	CDS	42..1175	
FT		/*tag= a	
FT		/product= "calendulic acid desaturase"	
XX	DE19941609-A1.		
PN			
XX	08-MAR-2001.		
PD			
XX	01-SEP-1999;	99DE-01041609.	
PF			
XX	01-SEP-1999;	99DE-01041609.	
PR			
XX	(IPBP-) IPB INST PFLANZENBIOCHEMIE.		
PA	Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;		
PI	WPI; 2001-283028/30.		
XX	P-PSDB; AAB70946.		
DR			
XX	New nucleic acid sequence encoding Calendula officinalis calendulic acid		
CC	desaturase, useful for e.g. producing transgenic plants having oil with		
CC	an increased unsaturated fatty acid content..		
PT	Claim 1b; Page 13-15; 22pp; German.		
XX	This invention describes a novel isolated nucleic acid sequence (I)		
CC	encoding a Calendula officinalis calendulic acid desaturase polypeptide.		
CC	The invention also describes (I) a process for producing unsaturated		
CC	fatty acids, comprising introducing at least one copy of (I) or (II) into		
CC	an oil-producing organism, growing the organism, isolating oil from the		
CC	organism and releasing fatty acids from the oil;(2) a process for		
CC	producing triglycerides with an increased unsaturated fatty acid content,		
CC	comprising introducing at least one copy of (I) or (II) into an oil-		
CC	producing organism, growing the organism and isolating oil from the		
CC	organism; (3) a process for producing saturated fatty acids, comprising		
CC	introducing at least one nonfunctional copy of (I) or (II) into an oil-		
CC	producing organism, growing the organism, isolating oil from the organism		
CC	and releasing fatty acids from the oil; (4) a process for producing		
CC	triglycerides with an increased saturated fatty acid content, comprising		
CC	introducing at least one nonfunctional copy of (I) or (II) into an oil-		
CC	producing organism, growing the organism and isolating oil from the		
CC	organism; (5) an enzyme capable of converting a diunsaturated fatty acid		
CC	of to a triunsaturated fatty acid. Transgenic organisms (especially		
CC	plants) containing one or more copies of (I) are useful for producing		
CC	oils with an increased unsaturated fatty acid content. Transgenic		
CC	organisms (especially plants) containing one or more nonfunctional copies		
CC	of (I) are useful for producing oils with an increased saturated fatty		
CC	acid content. (I) and fragments of (I) are also useful for isolating		
CC	genomic sequences by homology screening. This sequence encodes the		



CC	calendulic acid desaturase described in the method of the invention
XX	
SQ	Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;
	Query Match 47.9%; Score 673; DB 4; Length 1285;
	Best Local Similarity 77.2%; Pred. No. 5.6e-157;
	Matches 833; Conservative 0; Mismatches 240; Indels 6; Gaps 1;
Qy	159 CGCAATTCCTGTTAAGTGATCTAAGAAAGCAATCCCTGCAATGCTTCGGCGATCCG 218
Db	112 CACCGTTACCGTTAAGCGATCTGAAGAAAGCGATTCCTTACCATTGCTTTGAGCGATCTG 171
Qy	219 CCGTCTGTCATCTGCTACGTAGTTTACAGGATCTCAATTCACCTTCCTTTTATACACGG 278
Db	172 TCATCCGGTCTCATPACTATGTTGTTCAATGATCTCAATTTGTCCTATGCTTCTACTACC 231
Qy	279 TCGCAACACCTACATTCCTCACCTCCCTCTCTCTAGTTTACTTACATGCGCGGTTT 338
Db	232 TTGCAAACACGTATATCCCTCTTATCTCTACACCTCTGGCTTACTAGCATGGCCGTTT 291
Qy	339 ACTGGTTTGGCAATCTTTGCATCTCTCACTGGTTTATGGGTCCTCGGCCATGAATCGGCC 398
Db	292 ACTGGTTTGTCAAGCTAGCATCTCTCACCGGCTCTGGGTCATCGGTCAAGAAATGTGGTC 351
Qy	399 ATCATGCCCTTTAGTGAGTACCAAGTGATTAACCGCGTTGGATTGCTCTCCATTCCG 458
Db	352 ACCATGCAATTTAGCGACTACCAAGTTGATTAATGATGTTGGAATGCTGTCTCATTCGG 411
Qy	459 CTCCTCTCACCCCTTACTTTTCTTGGAAATACAGCCATCGAAAGCACCATCGAAACAA 518
Db	412 CTCCTCTCACCCCGTATTTCTTGGAAATATAGCCAGGAAATCACACCGCCACAA 471
Qy	519 ATTCACTCGAAAGAGGAAAGTTTACATCTCTAGAACTCAGTCCAGCTCAGGACTTACT 578
Db	472 ATTCACTCGATAACGATGAAGTTTACATTTCTTAAACGTAAGTCGAAGGTCGAAGTTTAT 531
Qy	579 CCACATACGAATTTCTTACAAACAGCCCTGTGTCGAACTCTCATCTTGGTTCATGTTAA 638
Db	532 CCA-----AATCTTTAAACAATCCACCCGGCGAGTGTTCACTTTGGTGTTCGGTTGA 585
Qy	639 CTTTAGGATTTCTTTATACCTCTTAAGCAATGTTTTCAGGCAAGAGTACGATGATTTA 698
Db	586 CTTTAGGATTTCCGTTATATCTTACTTAATATCTCGGCCAAGAAATACGGGAGTTTG 645
Qy	699 CCAACCACTTTGATCCATTGAGCCCGATCTTCAACCGAGCGTGAGGAAATCCAGGTTGCGT 758
Db	646 CCAACCACTTTGATCCCATGAGTCCAAATTTTCAACGATCGTGAACGCGTTCAAGTTTTCG 705
Qy	759 TATCAGATCTTGGTATCGTTGCGAGTGTTTTACGGACTCAAGTTTCTTCTTACAAACAAG 818
Db	706 TATCCGATTTCCGTTCTTCTCGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAG 765
Qy	819 GATTTGGTGGGTGATGTGCATGTATGGAGTTTCCAGTGATAGGTCTGAAATTCCTTCATTA 878
Db	766 GGGCAGCTTGGGTAATCAACATGACGCAATTCAGTACTAGGTGTAAAGCGTGTCTTCG 825
Qy	879 TCGTAATCACTTATCTGCACACACACATCTGTCTCTACCCCATTAACGATTCACACCGAAT 938
Db	826 TTTTGTATCACATATTTGCAACACACCCATCTCTACTCCCTCATTTATGATTCACACCGAAT 885
Qy	939 GGAATCGGATCAAGAGGCGTTGACCAATCGACAGAGATTTCCGTTCTCTGTAATCCGG 998
Db	886 GGAATCGGATCAAGAGGCGCTTATCAACAAATCGATAGGGAATTTCCGGTTCCTGAAATCCGG 945
Qy	999 TTTTCCAGAGCTTACACACACCCACGTTGTGCAACATTTGTTTCCCTACATTCACATTT 1058
Db	946 TTTTCCAGAGCTTACACACACTCAAGCTTGTGATCATTTGATCTCATACATTCACATTT 1005
Qy	1059 ATCATGCAAGAGGCAAGCGAGGCGATCAAGCCAAATCTTGGGTGATTTACAGGATGATCG 1118
Db	1006 ATCATGCAAGAGGCAAGGAGTGAATCAAGCCAGTGTGTGGCGGAGTACTATAAATCG 1065
Qy	1119 ACAGGACTCCATTTTTCAAAGCAATGTGAGAGAGAGGCCAAGGAATGCAATTTTACATCGAGC 1178

Db	1066 ACAGGATCCAAATTTTCAAGCATATGTATAGAGAGGCTAAGGATGCATCTACATCGAGC 1125
Qy	1179 AAGATGCAGACAGCAAGCAAAAGGACATATTGTTACCTACCAATAAATGTAATCGATGATG 1237
Db	1126 CCGATGAGGATAGCGAGCACAAGAGTGTGTTCTGTTACCAACAGATGTAATCAAAAAGG 1184
RESULT 8	
ADR87352	
ID	ADR87352 standard; cDNA; 1134 BP.
XX	
AC	ADR87352;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Codon optimised hydroxylase/ epoxigenase coding sequence, SEQ ID 33.
XX	
KW	Nematocide; Plant; 16C monounsaturated fatty acid;
KW	18C monounsaturated fatty acid; 20C monounsaturated fatty acid;
KW	fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;
KW	acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;
KW	hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
KW	nematode; gene; ss.
XX	
OS	Stokesia laevis.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	1..1134
FT	/*tag= a
FT	/product= "Codon optimised Hydroxylase/ epoxigenase"
XX	
PN	WO2004071168-A2.
XX	
PD	26-AUG-2004.
XX	
PF	04-FEB-2004; 2004WO-US003254.
XX	
PR	05-FEB-2003; 2003US-0445293P.
XX	
PA	(DIVE-) DIVERGENCE INC.
XX	
PI	Verbsky MU, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;
PI	Hresko MC, McIaird MB, Zentella R;
XX	
DR	WPI; 2004-634973/61.
DR	P-PSDB; ADR87361.
XX	
PT	Novel transgenic plant containing DNA construct having nucleic acid
PT	encoding polypeptide for catalyzing conversion of substrate to
PT	monounsaturated fatty acid product, useful for controlling nematodes.
XX	
PS	Claim 74; SEQ ID NO 33; 180pp; English.
XX	
CC	The present invention relates to transgenic plants (I) containing one or
CC	more DNA constructs. The DNA constructs have a nucleic acid encoding a
CC	protein effective for catalyzing the conversion of a substrate to a 16C,
CC	18C or 20C monounsaturated fatty acid product, e.g. a fatty acid
CC	epoxigenase or a fatty hydroxylase, and a regulatory element operably
CC	linked to the nucleic acid encoding the protein, where the regulatory
CC	element confers expression in vegetative tissue of the plant. The fatty
CC	acid epoxigenase or a fatty hydroxylase can be
CC	phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol
CC	acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty
CC	acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in
CC	a vegetative tissue. The DNA construct of (I) is useful in the production
CC	of hydroxylases and epoxigenases that controls nematode damage in
CC	commercially important plant species and so (I) exhibits increased
CC	resistance to nematodes. (I) provides an effective, environmentally safe
CC	methods of inhibiting nematode metabolism, growth, viability,
CC	development, infectivity and/or the nematode life cycle. (I) provides
CC	season-long nematode control, thus providing labor savings, by reducing





CC exemplification of the present invention.

Sequence 1134 BP; 299 A; 259 C; 225 G; 351 T; 0 U; 0 Other;

Query Match 47.3%; Score 665.6; DB 14; Length 1134;  
Best Local Similarity 77.1%; Pred. No. 3.8e-155;  
Matches 825; Conservative 0; Mismatches 239; Indels 6;

	Matches	825	Conservative	0	Mismatches	239	Indels	6	Gaps	1
Qy	159	CGCCATTTCTCGTTAAGTGATCTAAAGAAAGCAATCCCTGTCACATTCCTTCGCGCATCCG	218							
Db	71	CACCTTTACATTAAGTGATATAAGAAAGCAATCCCTCCCAATGCTTCAAAAGGCTG	130							
Qy	219	CCGTCTGGTCATCTCTGCTACGTAGTTCAGGATCTCATTTACACCTTCCTTTTATACACGG	278							
Db	131	TCATAAGGTCCTTCATATATATGTGTTTCATGATCTCATGCTCTCTCATGCTCTTCCTTC	190							
Qy	279	TGCGCAACACCTACATTCCTCACCTCCCTCCTCCTAGTTTATCTTAGCATGGCCGGTTT	338							
Db	191	TCGCAACTACATATATTACTGTTCTTCTGCTCTCTTGTCTTATATAGCTTGGCCAGTTT	250							
Qy	339	ACTGGTTTTCGCAATCTTTGCATCTCACTGGTTTATAGGGTCTCTCGGCCATGAATTCGGGCC	398							
Db	251	ACTGGTTTTCGCAAGCAAGTATTCTCACTGGGTTGTTGGGTTATCGGCCATGAATGTGTC	310							
Qy	399	ATCATGCTTTTAGTGAGTTACAGTGGATTTGATAGCGCGTTGGATTCGTCTCTCATTTCCG	458							
Db	311	ACCATGCTTTTAGTGAATACCAAGTGGATTTGATGACACAGTTTGGGTTTCATCTCCACTCTG	370							
Qy	459	CTCTCTCCACCCCTTACTTTTCTTTGGAAATACAGCCATCGAAAGCAACCATCGAAACACAA	518							
Db	371	CTCTCTCCACCCCTTACTTTCTTTGGAAATATAGCCATAGGAATCACCATGCTTAACAA	430							
Qy	519	ATTCATTCGAAAAAGGAGGTTTACATTCCTAGAACTCATGCTCCAGCTCAGGACTTACT	578							
Db	431	ATTCATTCGAAAGGAGGTTTACATTCCTTAAGAGGAAATCCAAAGTCAAGACTTACT	490							
Qy	579	CCACATACGATTTCTTGACAAACGCGCTGGTCGAACTCTCATCTTGGTCTCATGTGTTAA	638							
Db	491	CCA-----AATCCTTAACAAACCCCTGGAAGGGTGTTCACCTTGGTTCAGGTGTA	544							
Qy	639	CTTTAGGATTTCTTTTATACCTCTTTAACGAATGTTTCAGGCAAGAAAGTACGATAGATT	698							
Db	545	CTCTAGGGTTTCCTTTGTACCTGTTTAACTAATATCTCTGGAAGAAATACCAAAGTTTG	604							
Qy	699	CCAAACCATTTTGATCCATTGAGCCGATCTTTCACCGAGCTGAGGGAATCCAGGTGGGT	758							
Db	605	CCAAACCATTTTGATCCATTGATGCCATCTTTCACCGAGAGGGAAGGAATTCAGGTCTTG	664							
Qy	759	TATCAGATCTTGGTATCGTTTCAGTGTGTTTACGAGCTCAAGTTCCTGTACAAACAAAG	818							
Db	665	TATCAGATCTTGGTCTTCTAGCTGTAACTTAGGCAATCAGCTTCTTGTGCTGGAAG	724							
Qy	819	GATTTGGTTGGGTGATGTGCATGTATGGAGTTCCAGTGATAGGCTGTGAATTCCTTCATTA	878							
Db	725	GAGCTGTCTGGTGCATGTCATCTATGAGTTCAGTCTTAGGTGAAGCGTGTCTTCTTCG	784							
Qy	879	TCGTAATCATTTATCTGCACACACACATCTGTCTGTCACCCCATTCAGATTCACCCGAT	938							
Db	785	TTTTTGATCAGTTTATCTGCACACACCCCATCTTCTCTGGCTCATTTACGATTCATCTGAT	844							
Qy	939	GGAACTGATCAAAAGGAGCTTGACCAATTCGACAGAGATTTTCGGTCTCTCGAATCGG	998							
Db	845	GGAACTGATCAGAGGGCATTTGCAACCATTCGATAGGGAATTTGGGTTCTTAATAGGG	904							
Qy	999	TTTTTCCAGCGTTTACACACCCACGTTGTTGCACCATTTGTTTCCCTACATTCACATT	1058							
Db	905	TTTTTCCATGACGTTTACACACACTCATGTATTGTCATCTTTTGATCTCTTACATTCACACT	964							
Qy	1059	ATCATGCAAGAGGCAAGCGAGCCATCAAGCCNATCTTGGGTGATTTACAGGATGATCG	1118							
Db	965	ATCATGCAAGAGGCAAGAGATGCAATCAAAACCAAGTTTGGGTGATTTATTAAGATTG	1024							
Qy	1119	ACAGGATCTCCATTTTTTCAAGCAATGTGGAGAGAGGCCAAGGAATGCATTTACATCGAGC	1178							

Db 1025 ATAGGACTCTTATTCAAAGCAATGTGGAGAGAGCCAAAGGAATGATCTATATCGAGC 1084  
 Qy 1179 AAGATGCAGACCAAGCACAAGCACAATATTGGTACCAATAAATGAA 1228  
 Db 1085 CAGATGAAGATACTGAACACAAAGGGTGTTCCTGCTGATACCAATAAATGTA 1134

RESULT 10  
 ADR87325  
 ID ADR87325 standard; cDNA; 1125 BP.  
 XX  
 AC ADR87325;  
 XX  
 XX 18-NOV-2004 (first entry)  
 DE Hydroxylase/ epoxxygenase coding sequence, SEQ ID 6.  
 XX  
 XX Nematocide; Plant; 16C monounsaturated fatty acid;  
 KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;  
 KW fatty acid epoxxygenase; fatty hydroxylase; phospholipid:diacylglycerol;  
 KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;  
 KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;  
 KW nematode; gene; ss.  
 XX  
 XX Crepis biennis.  
 OS  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..1125  
 FT /\*tag= a  
 FT /product= "Hydroxylase/ epoxxygenase"  
 XX  
 XX WO2004071168-A2.  
 XX  
 XX  
 PD 26-AUG-2004.  
 XX  
 XX 04-FEB-2004; 2004WO-US003254.  
 XX  
 XX 05-FEB-2003; 2003US-0445293P.  
 XX  
 XX (DIVE-) DIVERGENCE INC.  
 XX  
 PA Verbsky ML, Baulite C, Williams DJ, Kloek AP, Davila-Aponte JA;  
 PI Hresko MC, McIaird MB, Zentella R;  
 XX  
 DR WPI: 2004-634973/61.  
 DR P-PSDB; ADR87337.  
 XX  
 PT Novel transgenic plant containing DNA construct having nucleic acid  
 PT encoding polypeptide for catalyzing conversion of substrate to  
 PT monounsaturated fatty acid product, useful for controlling nematodes.  
 XX  
 PS Claim 74; SEQ ID NO 6; 180pp; English.  
 XX  
 CC The present invention relates to transgenic plants (I) containing one or  
 CC more DNA constructs. The DNA constructs have a nucleic acid encoding a  
 CC protein effective for catalyzing the conversion of a substrate to a 16C,  
 CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid  
 CC epoxxygenase or a fatty hydroxylase, and a regulatory element operably  
 CC linked to the nucleic acid encoding the protein, where the regulatory  
 CC element confers expression in vegetative tissue of the plant. The fatty  
 CC acid epoxxygenase or a fatty hydroxylase can be  
 CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol  
 CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty  
 CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in  
 CC a vegetative tissue. The DNA construct of (I) is useful in the production  
 CC of hydroxylases and epoxxygenases that controls nematode damage in  
 CC commercially important plant species and so (I) exhibits increased  
 CC resistance to nematodes. (I) provides an effective, environmentally safe  
 CC method of inhibiting nematode metabolism, growth, viability,  
 CC development, infectivity and/or the nematode life cycle. (I) provides  
 CC season-long nematode control, thus providing labor savings, by reducing  
 CC the need for and frequency of chemical control. The present sequence is



CC plant is useful in preparing compounds having anthelmintic activity. The  
CC present sequence encodes an epoxigenase which is used in the  
CC exemplification of the present invention.

Sequence 1125 BP; 285 A; 277 C; 234 G; 329 T; 0 U; 0 Other;











CC including coating, composites, adhesives and plasticizers. The present  
CC sequence is the Crepis palustris epoxysenase cDNA. Note: The present  
CC sequence is described as SEQ ID NO:10 in the sequence listing. But SEQ ID  
CC NO:12 on the page 2 of the specification.

XX  
SQ Sequence 1344 BP; 344 A; 308 C; 278 G; 414 T; 0 U; 0 Other;

Query Match 45.5%; Score 640.4; DB 14; Length 1344;  
Best Local Similarity 75.5%; Pred. No. 7.3e-149;  
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTCGCGCGCATTCCTCGTTAAAGTATCTAAAGAAAGCAATCCCT 196  
DB 75 GAACGTGTCTCAGTTGATCCAGTAACCTTCCTACGTAGTGAATTGAAGCAAGCAATCCCT 134

QY 197 GCACATTGCTTCGCGCGATCGCGCTCTGGTTCATCTGCTACGTAGTTACAGATCTCAT 256  
DB 135 CCCATTGCTTCGAGATCTGTAATCGCTCATCTTACTATGTTGTTCAAGATCTCAT 194

QY 257 ATCACCTTCCTTTTATACACGGTGGCGAAGCACTACATTCCTCAGCTCCCTCCCTCCTA 316  
DB 195 ATTGCCTACATCTTCTACTCTTCTGCAACACATATATCCCTACTCTTCTCTACTAGTCTA 254

QY 317 GTTACTTAGCATGCGCGTTTACTGTTTTCGCAATCTTCATCTCTCACTGGTTTATGG 376  
DB 255 GCCTACTTAGCTTGGCCCGTTTACTGGTTCGTCAAGCTAGGCTCTCATCTGGCTTATGG 314

QY 377 GTCCTCGGCCATGAATCGGCCATCATGCTTTAGTGTAGTACCAGTGGATTGATAACGCC 436  
DB 315 ATCCTCGGCCAAGATGGTCAACATGCTTTAGCACTACACATGGTTTGACGACACT 374

QY 437 GTTGAATTCGTCCTCCATTCGGCTCTCTCACTCCCTTACTTTTCTTGGAAATACAGCCAT 496  
DB 375 GTGGCTTCATCTCTCACTCATTTCTCTCTCACTCCCGTATTTCTCTTGGAAATTCAGTCA 434

QY 497 CGAAGACACCATGCAACACAAATTCCTCGAAGACAGGAGTTTACATTCCTAGAACT 556  
DB 435 CGGAATACCATTCGCAACACAAATTCCTCGAAGACAGGAGTTTACATTCCTAGAAAGC 494

QY 557 CAGTCCCAAGCTCAGGACTTACTCCACATACGAATTTCTTGACACACACCGCTGGTCAATC 616  
DB 495 AAGTCCAAACTCGCGGT-----ATCTATAAATCTTTAACAACCCACCTGGTGGGCTG 548

QY 617 CTCATCTTGGTCAATGTTAACTTAGGATTTCTTTATACCTCTTAAAGAAATGTTTCA 676  
DB 549 TTGGTTTGAATATCATGTTCACTCTAGGATTTCTTTATACCTCTTGACAAATATTTCC 608

QY 677 GGCAGAAAGTACGATAGATTTACCAACCATTTGATCCATTGAGCCGATCTTCAACCGAG 736  
DB 609 GGCAGAAATACGACAGGTTTGCCAAACCATTCGACCCCATGATGTCATTTTCAAGAA 668

QY 737 COTGAGCGAATCCAGTTGCGTTATCAGATCTTGGTATCGTTGACAGTGTTTTACCGACTC 796  
DB 669 CGTGAGCGGTTTCAGGTTCTCTCTTCGATCTTGGTCTTCTTGCGGTGTTTATGGAAT 728

QY 797 AAGTTTCTGTACAAACAAAGGATTTGGTTGGGTGATGTGATGTATGGAGTTCCAGTG 856  
DB 729 AAAGTTGCTGTAGCAAAATAAGGAGCTGCTTGGGTAGCGTGCATGTATGGAGTTCCGGTA 788

QY 857 ATAGTCTGAATTCCTTCAATTCATTCATCTTATCTGACCAACACATCTGTCGTCA 916  
DB 789 TTAGGCGTATTTTACCTTTTTCATGTGATCACCTTCTTGACCAACACCATCAGTCGTG 848

QY 917 CCCCAATTACGATTCACCGAATGGAACTGGATCAAGAGGCGCTTGACCAATCGACAGA 976  
DB 849 CCTCATTTATGATTTCACTGAATGGAATGGATCAGAGGGGCTTCTCAGCAATCGATAGG 908

QY 977 GATTTCCGTTCTCTGAATCGGGTTTTCACGAGGTTACACACCGCATGTTGACCAT 1036  
DB 909 GACTTTGGATTCCTGAATAGTGTGTTTCCATGATGTTTACACACATCATGTTCATGATCAT 968

QY 1037 TTGTTTCCCTACATTCACATTCATTCATGCAAGGAGGCAAGCGGCGCATCAAGCCAATC 1096

Search completed: September 25, 2006, 00:17:02  
Job time : 1366 secs

Db 969 TTGTTTTTCATACATTCACACTATCATGCAAGGAGGCAAGGATGCAATCAAGCCAATC 1028  
QY 1097 TTGGGTGATTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATGTGGAGAGAGGCC 1156  
DB 1029 TTGGGCGACTTTTATATGATCGACAGGACTCCATTTTAAAGCAATGTGGAGAGAGGCC 1088  
QY 1157 AAGGAATGCATTTTACATCGAGCAAGATGCGACAGCAAGCAAGGACATATTGGTAC 1216  
DB 1089 AGGAGTGCATGTACATCGAGC-----CTGATAGCAAGCTCAAGGTGTTTATTGGTAT 1142  
QY 1217 CATAAAATGTAATC 1230  
DB 1143 CATAAATTTGATC 1156

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:55:37 ; Search time 183 Seconds  
(without alignments)  
956.804 Million cell updates/sec

Title: US-10-622-774-2

Perfect score: 2086  
Sequence: 1 MSDSYDDRMKDHMDERAPI.....IYIEQDADSKHKGTWYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2086	100.0	378	US-10-622-774-2	Sequence 2, Appli
2	2077	99.6	378	US-10-912-534-136	Sequence 136, Appl
3	1549.5	74.3	377	US-10-772-227-36	Sequence 36, Appl
4	1549.5	74.3	377	US-10-772-227-38	Sequence 38, Appl
5	1549.5	74.3	377	US-10-772-227-42	Sequence 42, Appl
6	1549.5	74.3	377	US-10-912-534-36	Sequence 36, Appl
7	1549.5	74.3	377	US-10-912-534-38	Sequence 38, Appl
8	1549.5	74.3	377	US-10-912-534-42	Sequence 42, Appl
9	1523.5	73.0	377	US-10-732-923-4878	Sequence 4878, Ap
10	1504	72.1	374	US-10-772-227-41	Sequence 41, Appl
11	1504	72.1	374	US-10-912-534-41	Sequence 41, Appl
12	1501	72.0	373	US-09-981-124-4	Sequence 4, Appli
13	1499	71.9	374	US-10-912-534-137	Sequence 137, Appl
14	1498	71.8	374	US-10-772-227-18	Sequence 18, Appl
15	1498	71.8	374	US-10-912-534-18	Sequence 18, Appl
16	1497	71.8	374	US-10-912-534-135	Sequence 135, Appl
17	1493	71.6	374	US-09-981-124-2	Sequence 2, Appli
18	1493	71.6	374	US-10-732-923-4887	Sequence 4887, Ap
19	1482	71.0	380	US-10-772-227-24	Sequence 24, Appl
20	1482	71.0	380	US-10-912-534-24	Sequence 24, Appl
21	1424.5	68.3	375	US-10-732-923-4836	Sequence 4836, Ap
22	1410	67.6	326	US-11-087-099-3460	Sequence 3460, Ap
23	1386	66.4	384	US-09-981-124-20	Sequence 20, Appl
24	1351	64.8	326	US-11-087-099-6724	Sequence 6724, Ap
25	1290.5	61.9	383	US-10-732-923-4841	Sequence 4841, Ap
26	1284.5	61.6	383	US-10-732-923-4840	Sequence 4840, Ap
27	1279	61.3	383	US-10-464-631-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-10-622-774-2  
; Sequence 2, Application US/10622774  
; Publication NO. US2005002270A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Kentucky Research Foundation  
; APPLICANT: Hildebrand, David  
; APPLICANT: Hatanaka, Tomoko  
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSYGENASE GENE  
; FILE REFERENCE: 050229-0377  
; CURRENT APPLICATION NUMBER: US/10/622,774  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 60/396,406  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Stokesia laevis  
US-10-622-774-2

Query Match	100.0%	Score 2086;	DB 5;	Length 378;
Best Local Similarity	100.0%	Pred. No. 1.7e-197;		
Matches	378;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MSDSYDDRMKDHMDERAPI	DPAPFSLDLKKAIPAHCFRRSAVMS	SCYVQDLITFFLL 60
Db	1	MSDSYDDRMKDHMDERAPI	DPAPFSLDLKKAIPAHCFRRSAVMS	SCYVQDLITFFLL 60
QY	61	YTVANTYI	PHLPPLVYLAWPYWFCQSCILGLWLG	HECGHAFSEYQWIDNAGFVL 120
Db	61	YTVANTYI	PHLPPLVYLAWPYWFCQSCILGLWLG	HECGHAFSEYQWIDNAGFVL 120
QY	121	HSALTPYFSWKYSHRKHANTNS	LENEBVIPTQSQRLTYSTYFELDNT	PGRIILVI 180
Db	121	HSALTPYFSWKYSHRKHANTNS	LENEBVIPTQSQRLTYSTYFELDNT	PGRIILVI 180
QY	181	MLTGLFPPLYLLTNVSGKKYDR	TNHPDPLSPFTRERERIQVALSD	LIGIVAVFYGLKFLVQ 240
Db	181	MLTGLFPPLYLLTNVSGKKYDR	TNHPDPLSPFTRERERIQVALSD	LIGIVAVFYGLKFLVQ 240
QY	241	TKGFGWCMYGVPIGLNSFIIV	ITYLHHTLSSPHYSTENWIKGALT	ITIDRDFGLL 300
Db	241	TKGFGWCMYGVPIGLNSFIIV	ITYLHHTLSSPHYSTENWIKGALT	ITIDRDFGLL 300
QY	301	NEVFDHVTHTVHLHLPPYI	PHYHKAKEASEAKPIILGDYRMID	RTPFPFKAMREACEY 360
Db	301	NEVFDHVTHTVHLHLPPYI	PHYHKAKEASEAKPIILGDYRMID	RTPFPFKAMREACEY 360

Qy 361 IEQDADSKHGTYWYHKM 378  
Db 361 IEQDADSKHGTYWYHKM 378

## RESULT 2

US-10-912-534-136  
; Sequence 136, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeke, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Deryck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Stokesia laevis B  
US-10-912-534-136

Query Match 99.6%; Score 2077; DB 5; Length 378;  
Best Local Similarity 99.5%; Pred. No. 1.3e-196;  
Matches 376; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDSVDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSVAVSSCVVQDLITFL 60  
Db 1 MASSYDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSVAVSSCVVQDLITFL 60  
Qy 61 YTVANTYIPLPPLVYLAWPVYVFCQSCILTLGLVGLGHCCHAFSEYQWIDNAGFVL 120  
Db 61 YTVANTYIPLPPLVYLAWPVYVFCQSCILTLGLVGLGHCCHAFSEYQWIDNAGFVL 120  
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIIPRTQSQLRTYSTYEFDLNTPGRILILVI 180  
Db 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIIPRTQSQLRTYSTYEFDLNTPGRILILVI 180  
Qy 181 MTLGFPYLLTNVSGKYYDRFTNHPDPLSPIFTRERIQVALSDLGIVAVFYGLKFLVQ 240  
Db 181 MTLGFPYLLTNVSGKYYDRFTNHPDPLSPIFTRERIQVALSDLGIVAVFYGLKFLVQ 240  
Qy 241 TKGFGVVMCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
Db 241 TKGFGVVMCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
Qy 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Db 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Qy 361 IEQDADSKHGTYWYHKM 378  
Db 361 IEQDADSKHGTYWYHKM 378

## RESULT 3

US-10-772-227-36  
; Sequence 36, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeke, Michelle L.  
; APPLICANT: Baublite, Catherine

; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Stokesia laevis  
US-10-772-227-36

Query Match 74.3%; Score 1549.5; DB 4; Length 377;  
Best Local Similarity 72.0%; Pred. No. 2.2e-144;  
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSVDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSVAVSSCVVQDLITFL 60  
Db 7 MSDLSGDK----NLKRVFVDP--PFTLSDDIKKAIAPPHCFKRSVIRSSYYVHDLIVSVF 61  
Qy 61 YTVANTYIPLPPLVYLAWPVYVFCQSCILTLGLVGLGHCCHAFSEYQWIDNAGFVL 120  
Db 62 FFLATTYITVLPAPLAYIAVPVYVFCQASILTGLVGLGHCCHAFSEYQWIDDTVGFIL 121  
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIIPRTQSQLRTYSTYEFDLNTPGRILILVI 180  
Db 122 HSALLTPYFSWKYSHRKHANTNSLENEEVIIPRTQSQLRTYSTYEFDLNTPGRILILVI 179  
Qy 181 MTLGFPYLLTNVSGKYYDRFTNHPDPLSPIFTRERIQVALSDLGIVAVFYGLKFLVQ 240  
Db 180 RLTLGFPYLLTNVSGKYYDRFTNHPDPLSPIFTRERIQVALSDLGIVAVFYGLKFLVQ 239  
Qy 241 TKGFGVVMCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
Db 240 AKGAVVTCIYGVPIGLNSFIIVTYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 299  
Qy 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Db 300 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 359  
Qy 361 IEQDADSKHGTYWYHKM 378  
Db 360 IEQDADSKHGTYWYHKM 377

## RESULT 4

US-10-772-227-38  
; Sequence 38, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeke, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130



```
Db 180 RLTLGPPLLYLTNLSGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKGFGWVMCMYGPVIGNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWVTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPILGDRYMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLSIYIPHYHAKSEARDAIKPVLGDYIKIDRTPIPKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYWYHKM 377

RESULT 7
US-10-912-534-38
; Sequence 38, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Stokesia laevis
US-10-912-534-38

Query Match 74.3%; Score 1549.5; DB 5; Length 377;
Best Local Similarity 72.0%; Pred. No. 2.2e-144;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCVVQDLIITELL 60
Db 7 MSDLSGDK----NLKRVFVDP-PFTLSDIKKAIPPHCFKRSVIRSSYVVHDLIVSVF 61
Qy 61 YTVANTYIPLPPLVYLAWPVYWFQCSILTLGLWLGHECGHAFSEYQWIDNNAVGVFL 120
Db 62 PFLATTYITVLPAPLAYIAWPVYWFQCSILTLGLWLGHECGHAFSEYQWIDDTVGFI 121
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFDNTPGRILILVI 180
Db 122 HSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYS--KILNPPGRVFTLVF 179
Qy 181 MLTLGFPPLLYLTNLSGKKYQRPANHPDPLSPFTTERERIQVALSDGLIVAVFYGLKFLVQ 240
Db 180 RLTLGFPPLLYLTNLSGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKGFGWVMCMYGPVIGNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWVTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPILGDRYMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLSIYIPHYHAKSEARDAIKPVLGDYIKIDRTPIPKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYWYHKM 377

RESULT 9
US-10-732-923-4878
; Sequence 4878, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
```

```
Db 360 IEPDEDTEHKGYWYHKM 377

RESULT 8
US-10-912-534-42
; Sequence 42, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Stokesia laevis
US-10-912-534-42

Query Match 74.3%; Score 1549.5; DB 5; Length 377;
Best Local Similarity 72.0%; Pred. No. 2.2e-144;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCVVQDLIITELL 60
Db 7 MSDLSGDK----NLKRVFVDP-PFTLSDIKKAIPPHCFKRSVIRSSYVVHDLIVSVF 61
Qy 61 YTVANTYIPLPPLVYLAWPVYWFQCSILTLGLWLGHECGHAFSEYQWIDNNAVGVFL 120
Db 62 PFLATTYITVLPAPLAYIAWPVYWFQCSILTLGLWLGHECGHAFSEYQWIDDTVGFI 121
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFDNTPGRILILVI 180
Db 122 HSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYS--KILNPPGRVFTLVF 179
Qy 181 MLTLGFPPLLYLTNLSGKKYQRPANHPDPLSPFTTERERIQVALSDGLIVAVFYGLKFLVQ 240
Db 180 RLTLGFPPLLYLTNLSGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKGFGWVMCMYGPVIGNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWVTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPILGDRYMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLSIYIPHYHAKSEARDAIKPVLGDYIKIDRTPIPKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYWYHKM 377

RESULT 9
US-10-732-923-4878
; Sequence 4878, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
```

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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 4878
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Calendula officinalis
US-10-732-923-4878

Query Match
Best Local Similarity 73.0%; Score 1523.5; DB 5; Length 377;
Matches 269; Conservative 45; Mismatches 54; Indels 7; Gaps 3;

QY 8 RMKD---HMDERAPIDPAPFSLDLKKAIPAHCFFRSASVWSSCYVQDIIITFLIYTV 63
DB 6 RMSDPSEGNILERVDPD-PTTSLDLKKAIPHCFFRSVIRSSYYVVDLIVAVFYFL 64
QY 64 NTYIYIPLPPLVYLAWPVYWCOSILTLGLWLGHECGHAFSEYQWIDNAGVFLHSA 123
DB 65 NTYIYIPLPPLVYLAWPVYWCOSILTLGLWLGHECGHAFSDYQIDIDVGFVLHSA 124
QY 124 LTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEIDNTPGRILILVMT 183
DB 125 LTPYFSWKYSHRKHANTNSLENEEVIPTQSKVKIYS--KLLNPPGGRVFLVPLT 182
QY 184 LGFPLVLLTNVSGKGYDRFTNHPDPLSPIFTRERERIOVALSDLGIVAVFYGLKFLVQTKG 243
DB 183 LGFPLVLLTNISGKGYRPFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIFKLLVAAKG 242
QY 244 FGWMCMGVVPIGLNSPIIYTLHHTLSSPHYDSTEWNIKALTIIDRDFGLLNRV 303
DB 243 AAWVINNYAIPVLGVSFFVFLIYTLHHTLSSPHYDSTEWNIKALSTIDRDFGLNRV 302
QY 304 FHDVTHVLHLPFVPIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIYIEQ 363
DB 303 FHDVTHVLHLSIYPIPHYHAKARDAIKPVLGEYKIDRTPIPKAMREAKECIYIEP 362
QY 364 DADSKHGTYWYHKM 378
DB 363 DEDSEHGVPWYHKM 377

RESULT 10
US-10-772-227-41
; Sequence 41, Application US/10772227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-772-227-41

Query Match
Best Local Similarity 72.1%; Score 1504; DB 4; Length 374;
Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 1 MSDSYDDRMKOHMDERAPIDPAPFSLDLKKAIPAHCFFRSASVWSSCYVQDIIITFLI 60
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPPHCFQSRVIRSSYYVVDLIIAIFY 60
QY 61 YTVANTYIPLPPLVYLAWPVYWCOSILTLGLWLGHECGHAFSEYQWIDNAGVFL 120
DB 61 YFLADKYIPLPAPLAYLAWPLYWFCQASILTGLWLGHECGHAFSEYQWDDTVGFMV 120
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEIDNTPGRILILVI 180
DB 121 HSFLTLTPYFSWKYSHRKHANTSSIDNDEVIPKSKKAL--TYKLLNPPGGRLLVMI 178
QY 181 MUTLGPPLVLLTNVSGKGYDRFTNHPDPLSPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240
DB 179 MFTLGPPLVLLTNISGKGYRPFANHFDPMSPIFKERERFQVLLSDFGLLAVFYGIKVA 238
QY 241 TKGFGWCMGVVPIGLNSPIIYTLHHTLSSPHYDSTEWNIKALTIIDRDFGLL 300
DB 239 KGAAWACMYGVPMLGVFTLFDIYTLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 301 NRVFHDVTHVLHLPFVPIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIY 360
DB 299 NSVFHDVTHVLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 361 IEQDADSKHGTYWYHKM 378
DB 359 IE--PDSKRGVYVYHKL 374

RESULT 11
US-10-912-534-41
; Sequence 41, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-912-534-41

Query Match
Best Local Similarity 69.0%; Pred. No. 6.9e-140;
Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 1 MSDSYDDRMKOHMDERAPIDPAPFSLDLKKAIPAHCFFRSASVWSSCYVQDIIITFLI 60
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPPHCFQSRVIRSSYYVVDLIIAIFY 60
QY 61 YTVANTYIPLPPLVYLAWPVYWCOSILTLGLWLGHECGHAFSEYQWIDNAGVFL 120
DB 61 YFLADKYIPLPAPLAYLAWPLYWFCQASILTGLWLGHECGHAFSEYQWDDTVGFMV 120
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEIDNTPGRILILVI 180
DB 121 HSFLTLTPYFSWKYSHRKHANTSSIDNDEVIPKSKKAL--TYKLLNPPGGRLLVMI 178
QY 181 MUTLGPPLVLLTNVSGKGYDRFTNHPDPLSPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240
DB 179 MFTLGPPLVLLTNISGKGYRPFANHFDPMSPIFKERERFQVLLSDFGLLAVFYGIKVA 238
QY 241 TKGFGWCMGVVPIGLNSPIIYTLHHTLSSPHYDSTEWNIKALTIIDRDFGLL 300
DB 239 KGAAWACMYGVPMLGVFTLFDIYTLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 301 NRVFHDVTHVLHLPFVPIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIY 360
DB 299 NSVFHDVTHVLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 361 IEQDADSKHGTYWYHKM 378
DB 359 IE--PDSKRGVYVYHKL 374

RESULT 11
US-10-912-534-41
; Sequence 41, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-912-534-41

Query Match
Best Local Similarity 69.0%; Pred. No. 6.9e-140;
Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 1 MSDSYDDRMKOHMDERAPIDPAPFSLDLKKAIPAHCFFRSASVWSSCYVQDIIITFLI 60
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPPHCFQSRVIRSSYYVVDLIIAIFY 60
QY 61 YTVANTYIPLPPLVYLAWPVYWCOSILTLGLWLGHECGHAFSEYQWIDNAGVFL 120
DB 61 YFLADKYIPLPAPLAYLAWPLYWFCQASILTGLWLGHECGHAFSEYQWDDTVGFMV 120
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEIDNTPGRILILVI 180
DB 121 HSFLTLTPYFSWKYSHRKHANTSSIDNDEVIPKSKKAL--TYKLLNPPGGRLLVMI 178
QY 181 MUTLGPPLVLLTNVSGKGYDRFTNHPDPLSPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240
DB 179 MFTLGPPLVLLTNISGKGYRPFANHFDPMSPIFKERERFQVLLSDFGLLAVFYGIKVA 238
QY 241 TKGFGWCMGVVPIGLNSPIIYTLHHTLSSPHYDSTEWNIKALTIIDRDFGLL 300
DB 239 KGAAWACMYGVPMLGVFTLFDIYTLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 301 NRVFHDVTHVLHLPFVPIPHYHAKASEAIKPILDGYRMDRTPPFKAMWREAKECIY 360
DB 299 NSVFHDVTHVLHHTLSSPHYDSTEWNIKALSAIDRDFGFM 298
QY 361 IEQDADSKHGTYWYHKM 378
DB 359 IE--PDSKRGVYVYHKL 374

RESULT 11
US-10-912-534-41
; Sequence 41, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-912-534-41

Query Match
Best Local Similarity 69.0%; Pred. No. 6.9e-140
```

QY 121 HSALLTPFSWKYSRKHANTNSLENEEVIPTQSQRLTYSTYEFDLNTPGRILLIUVI 180  
DB 121 HSFLLTPTFSWKYSRHNHANTSSIDNDEVIPKSKSLAL--TYKLLNPPGRLLVMVI 178  
QY 161 MLTGLFPYLLTNVSGKYDRFTNHPDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQ 240  
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QY 241 TKGFQVNMCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
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QY 301 NRVFHDVTHVHLHLPYIPHYHAKESAEIKPILGDYRMDIRTPFFKAMWREAKECIY 360  
DB 299 NSVFHDVTHVHMHMFYSIPHYHAKESAEIKPILGDYRMDIRTPFFKAMWREAKECMY 358  
QY 361 IEQDADSKHKGTWYVHKM 378  
DB 359 IE--PDSKRKGVYVYHKL 374

RESULT 12  
US-09-981-124-4  
; Sequence 4, Application US/09981124  
; Patent No. US20020166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN METABOLISM  
; FILE REFERENCE: 26-98A  
; CURRENT APPLICATION NUMBER: US/09/981,124  
; PRIOR FILING DATE: 2003-10-17  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Crepis sp.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (292)..(292)  
; OTHER INFORMATION: The 'Xaa' at location 292 stands for Arg, or Ser.  
; NAME/KEY: misc\_feature  
; LOCATION: (937)..(937)  
; OTHER INFORMATION: N is any nucleotide residue  
; NAME/KEY: misc\_feature  
; LOCATION: (901)..(901)  
; OTHER INFORMATION: N is any nucleotide residue  
US-09-981-124-4

Query Match 72.0%; Score 1501; DB 3; Length 373;  
Best Local Similarity 71.3%; Pred. No. 1.4e-139;  
Matches 259; Conservative 48; Mismatches 52; Indels 4; Gaps 2;  
QY 16 ERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYVANTYIPHLPPPL 75  
DB 15 ERVSDVPVTFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYVANTYIPHLPPPL 74  
QY 76 VYLANPVYVFCQSCILTLGLVILGHECGHAFSEYQWIDNAVGVLSALLTPFSWKYSYH 135

DB 75 AYLANPVYVFCQSCILTLGLVILGHECGHAFSEYQWIDNAVGVLSALLTPFSWKYSYH 134  
QY 136 RKHANTNSLENEEVIPTQSQRLTYSTYEFDLNTPGRILLIUVI 195  
DB 135 RNHSNTSSIDNDEVIPKSKSLK--RIYKLLNPPGRLLVIMFTLGFPYLLTNIS 192  
QY 196 GKXYDRFTNHPDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQTKGFQVNMCMYGVPI 255  
DB 193 GKXYDRFANHPDPMSPFKERERFQVLSLGLLAVFYGLKFLVQVAVKAAWACVMYGVPI 252  
QY 256 IGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLLNVFHDVTHVHLH 315  
DB 253 LGVTFDFVITFLHHTQSSPHYDSTENWIRGALSALDXDFGLNSVFDVTHVHMH 312  
QY 316 LFPYIPHYHAKESAEIKPILGDYRMDIRTPFFKAMWREAKECIYIEODASKHKGTWY 375  
DB 313 LFSYIPHYHAKESAEIKPILGDYRMDIRTPFFKAMWREAKECIYIE--PDSKLGKVYVY 370  
QY 376 HKM 378  
DB 371 HKL 373

RESULT 13  
US-10-912-534-137  
; Sequence 137, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Kloeck, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Desyck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 137  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Crepis biennis  
US-10-912-534-137

Query Match 71.9%; Score 1499; DB 5; Length 374;  
Best Local Similarity 68.8%; Pred. No. 2.2e-139;  
Matches 260; Conservative 51; Mismatches 63; Indels 4; Gaps 2;  
QY 1 MSDSYDDRMKDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFL 60  
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFL 60  
QY 61 YTVANTYIPHLPPYLLVLANPVYVFCQSCILTLGLVILGHECGHAFSEYQWIDNAVGV 120  
DB 61 YFLADKYIPIPLPAPLAYLANPVYVFCQSCILTLGLVILGHECGHAFSEYQWIDNAVGV 120  
QY 121 HSALLTPFSWKYSRKHANTNSLENEEVIPTQSQRLTYSTYEFDLNTPGRILLIUVI 180  
DB 121 HSFLLTPTFSWKYSRHNHANTSSIDNDEVIPKSKSLAL--TYKLLNPPGRLLVMVI 178  
QY 181 MLTGLFPYLLTNVSGKYDRFTNHPDPLSPFTFERRERIOVALSDLGIVAVFYGLKFLVQ 240  
DB 179 MFTLGFPYLLTNISGKYDRFANHPDPMSPFKERERFQVLLSDGLLAVFYGLKFLVQ 238  
QY 241 TKGFQVNMCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300



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Db 239 KKGAAWVACWGVGMLGVFTLFDIITLHHTHOSPHYDSTWNNWIRGALSADRDGFM 298
Qy 301 NRVFHDVTHVHLHLPYIPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECY 360
Db 299 NSVFHDVTHVHWHHMFSPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECY 358
Qy 361 IEQADSKHGKGYWYHKM 378
Db 359 IE--PDSKRKGWYWHKL 374
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## RESULT 14

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US-10-772-227-18
; Sequence 18, Application US/1077227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Crepis biennis
US-10-772-227-18
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Query Match 71.8%; Score 1498; DB 4; Length 374;
Best Local Similarity 71.1%; Pred. No. 2.7e-139;
Matches 258; Conservative 48; Mismatches 53; Indels 4; Gaps 2;

Qy 16 ERAPIDPAPFSLDLKKAIPAHCRRSAVWSSCYVQDLIIITFLTYTANTYIPIPLPPL 75
Db 16 ERVSDVPFVPSLDLQAIPPHCFQSRVIRSSYVVHDLIIAIFYFLADKIPIPLPAPL 75
Qy 76 VYLAWPVWFQSCILITGLWVILGHECHHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Db 76 AYLAWPLYWFCQASILTGLWILGHECHHAFSEYQWVDDTVGFMVHSFLLTPYFSWKYSH 135
Qy 136 RKHANTNSLENEEVIPRTQSLRTYSTYEPDLNTPGRLIILVIMLTGLGFLYLLTNVS 195
Db 136 RNHANTSSIDNDEVIPKSKLAL--TYKLLNPPGRLVIMVIMFTLGFPLYLLTNIS 193
Qy 196 GKXYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFWNVMCMYGV 255
Db 194 GKXYDRFANHFDPMSPIFKERERFVLLSDGLLAVFYGIKVAVAKGAACVACMYGVPM 253
Qy 256 IGLNSFIIVITLHHTHSSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 315
Db 254 LGVFTLFDIITLHHTHOSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 313
Qy 316 LFPYIPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECYIEQADSKHGKGYWY 375
Db 314 MFSYIPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECYIE--PDSKRKGWYWY 371
Qy 376 HKM 378
Db 372 HKL 374
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## RESULT 15

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US-10-912-534-18
; Sequence 18, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Crepis biennis
US-10-912-534-18
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Query Match 71.8%; Score 1498; DB 5; Length 374;
Best Local Similarity 71.1%; Pred. No. 2.7e-139;
Matches 258; Conservative 48; Mismatches 53; Indels 4; Gaps 2;

Qy 16 ERAPIDPAPFSLDLKKAIPAHCRRSAVWSSCYVQDLIIITFLTYTANTYIPIPLPPL 75
Db 16 ERVSDVPFVPSLDLQAIPPHCFQSRVIRSSYVVHDLIIAIFYFLADKIPIPLPAPL 75
Qy 76 VYLAWPVWFQSCILITGLWVILGHECHHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Db 76 AYLAWPLYWFCQASILTGLWILGHECHHAFSEYQWVDDTVGFMVHSFLLTPYFSWKYSH 135
Qy 136 RKHANTNSLENEEVIPRTQSLRTYSTYEPDLNTPGRLIILVIMLTGLGFLYLLTNVS 195
Db 136 RNHANTSSIDNDEVIPKSKLAL--TYKLLNPPGRLVIMVIMFTLGFPLYLLTNIS 193
Qy 196 GKXYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFWNVMCMYGV 255
Db 194 GKXYDRFANHFDPMSPIFKERERFVLLSDGLLAVFYGIKVAVAKGAACVACMYGVPM 253
Qy 256 IGLNSFIIVITLHHTHSSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 315
Db 254 LGVFTLFDIITLHHTHOSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 313
Qy 316 LFPYIPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECYIEQADSKHGKGYWY 375
Db 314 MFSYIPHYHAKSEAIKPIIGDYRMDIDRTFFPKAMWREACECYIE--PDSKRKGWYWY 371
Qy 376 HKM 378
Db 372 HKL 374
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Job time : 184 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2006, 22:40:43 ; Search time 8116 Seconds  
(without alignments)  
11078.126 Million cell updates/sec

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Perfect score: 1406  
Sequence: 1 gtaggtttggtgcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_env.\*
- 2: gb\_pat.\*
- 3: gb\_ph.\*
- 4: gb\_pl.\*
- 5: gb\_pr.\*
- 6: gb\_ro.\*
- 7: gb\_sts.\*
- 8: gb\_sy.\*
- 9: gb\_un.\*
- 10: gb\_vi.\*
- 11: gb\_ov.\*
- 12: gb\_hcg.\*
- 13: gb\_in.\*
- 14: gb\_om.\*
- 15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1406	100.0	1406	4	AY462108 Stokesia
2	870	61.9	1364	2	AR064128 Sequence
3	673	47.9	1152	4	AJ245938 Calendula
4	673	47.9	1285	2	AX089471
5	664.8	47.3	1419	4	AY166773
6	657.6	46.8	1312	2	BD061165
7	657.6	46.8	1312	2	AR367438
8	657.6	46.8	1312	2	AX031162
9	641.6	45.6	979	4	AY166777
10	640.4	45.5	1358	2	BD061164
11	640.4	45.5	1358	2	CS023935
12	640.4	45.5	1358	2	CS023931
13	640.4	45.5	1358	2	CS023971
14	640.4	45.5	1358	2	AR367437
15	640.4	45.5	1358	2	AX031160
16	640.4	45.5	1358	4	CPY16283
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18	612.8	43.6	1435	2	CS023943

19	612.8	43.6	1435	2	CS023949	Sequence
20	612.8	43.6	1435	4	CAY16285	Y16285 Crepis alpi
21	611.2	43.5	979	4	AY166776	AY166776 Rudbeckia
22	602.4	42.8	979	4	AY166778	AY166778 Helichrys
23	487	34.6	1587	4	AY525163	AY525163 Cucurbita
24	483.6	34.4	1152	4	DQ157776	DQ157776 Jatropa
25	481.8	34.3	1507	4	AF188264	AF188264 Vernonia
26	478.8	34.1	1475	4	AF188263	AF188263 Vernonia
27	472.6	33.6	110900	4	AF066377	AF066377 Lotus cor
28	468	33.3	1516	4	AF525534	AF525534 Vernicia
29	467.8	33.3	1622	4	AY780572	AY780572 Tropaeolu
30	467.6	33.3	1152	4	DQ023609	DQ023609 Hevea bra
31	465.6	33.1	1291	4	AF074324	AF074324 Borago of
32	461.4	32.8	69947	4	AC166091	AC166091 Glycine m
33	456.4	32.5	1397	4	AJ879071	AJ879071 Capsicum
34	453.2	32.2	1314	4	AB188252	AB188252 Glycine m
35	448.6	31.9	1219	4	AF071892	AF071892 Prunus ar
36	445.4	31.7	1259	4	AF251844	AF251844 Helianthu
37	445.4	31.7	1452	4	AY083163	AY083163 Olea euro
38	445	31.7	1195	4	AY802998	AY802998 Helianthu
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41	445	31.7	1195	4	AY803001	AY803001 Helianthu
42	445	31.7	1195	4	AY803002	AY803002 Helianthu
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ALIGNMENTS

RESULT 1  
AY462108  
LOCUS AY462108 1406 bp mRNA linear PLN 03-DEC-2003  
DEFINITION Stokesia laevis delta 12 fatty acid epoxxygenase mRNA, complete cds.  
ACCESSION AY462108  
VERSION AY462108.1 GI:38564775  
KEYWORDS  
SOURCE Stokesia laevis  
ORGANISM Stokesia laevis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Vernoniaeae; Stokesia.  
1 (bases 1 to 1406)  
Hatanaka,T. and Hildebrand,D.F.  
Expression of a Stokesia laevis Epoxxygenase Gene  
Unpublished  
2 (bases 1 to 1406)  
Hatanaka,T. and Hildebrand,D.F.  
Direct Submission  
Submitted (10-NOV-2003) Plant Resource Science, Kobe University,  
1-1 Rokkodai, Nada, Kobe, Hyogo 657-8501, Japan

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/product="delta 12 fatty acid epoxxygenase"  
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/db\_xref="GI:38564776"  
/translation="MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAV  
WSSCYVQDLITFLTYVANTYIPLHPPPLVILAWPYWFCQICILGLWVLGECG  
HFAFSEYQWIDNAGFVLHSAITLTPFSWKYSHRKHANTVSLNEEYIIPRTOSQLR  
TYSYFELNDTPGRILILVIMLTGFFPLYLITNVSQKGYDLNFTSLFTFERER  
IQVALSDLGIVAVFYGLKFLVOTKGFQWCMYGPVIGLNSFTIIVIFLHHTLSSP  
HYDSTERNWIKGALTIDRDRGLNRPVPHDVTHTVLHLFPYIHYHKAESAIAKP  
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ORIGIN

Query Match		100.0%; Score 1406; DB 4; Length 1406;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Qy	61	GGATTTTTCAGAAATCTGGGAGAAAGGTAGCAGAAATGTGCGAATTCATATGATGATCGAATGAA 120
Db	61	GGATTTTTCAGAAATCTGGGAGAAAGGTAGCAGAAATGTGCGAATTCATATGATGATCGAATGAA 120
Qy	121	AGATCATGATATGACGAAACGAGCCCGGATGATCGCGCGCATTCGCTTAAAGTATCT 180
Db	121	AGATCATGATATGACGAAACGAGCCCGGATGATCGCGCGCATTCGCTTAAAGTATCT 180
Qy	181	AAAGAAAGCAATCCCTGCACATTCCTTCGCGCGATCGCGCTCTGGTCATCCTCGTACGT 240
Db	181	AAAGAAAGCAATCCCTGCACATTCCTTCGCGCGATCGCGCTCTGGTCATCCTCGTACGT 240
Qy	241	AGTTTCAGGATCTCATTAATACCTTCCTTTTATACACGGTCGCCAACACCTACATTCCTCA 300
Db	241	AGTTTCAGGATCTCATTAATACCTTCCTTTTATACACGGTCGCCAACACCTACATTCCTCA 300
Qy	301	CCTCCCTCCTCCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCCAACTTTCGAT 360
Db	301	CCTCCCTCCTCCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCCAACTTTCGAT 360
Qy	361	CCTCACTGGTTTATGGTTCCTCGGCCATGAATCGGCCATCATGCCCTTAGTGAGTACCA 420
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Qy	781	AGTGTTTTACGGAATCAAGTTTCTTGTAACAAACAAAGGATTTGGTTGGGTGATGTGAT 840
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Qy	841	GTAATGAGTTCCAGGTAGTGTGAATTCCTTCATATCGTAATCACTTATCTGCAACA 900
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Qy	901	CACACATCTGTCGTCACCCCATTAGGATTCACCGAATGGAATCGGATCAAGGAGCCCT 960
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Qy	961	GACCACATCGACAGAGATTTCCGTCCTCGTAATCGGGTTTTCCACGACGTTTACACAC 1020
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Qy	1021	CCACGTGTTGCACCATTTGTTCCCTACATTCACATTTATCATGCAAGGAGGCAAGCGA 1080
Db	1021	CCACGTGTTGCACCATTTGTTCCCTACATTCACATTTATCATGCAAGGAGGCAAGCGA 1080
Qy	1081	GGCCATCAAGCCCAATCTTGGGTGATTCACGAGTATCGCAGGACTCCATTTTTCRAAGC 1140
Db	1081	GGCCATCAAGCCCAATCTTGGGTGATTCACGAGTATCGCAGGACTCCATTTTTCRAAGC 1140
Qy	1141	AATGTGAGAGAGGCGCAAGGAATGCAATTTATCATCGAGCAAGATGCAGACAGCAACAA 1200
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Qy	1201	AGGACATATTTGCTTACCATTAATGTAATCGATGATGGAGTTAGTTTGGAAATAATGACA 1260
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Qy	1261	TGCAGCATCCCTTTTGTATCGTTCGAATCGTTCATTTCTTTATATGTTTTGTAAAGTAAA 1320
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Qy	1321	TAAATTAATCTTTGAGTGAAGATGGGAGCAGGAAACAGCAGCAATATATACGCTAAAA 1380
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DEFINITION	Sequence 3 from patent US 5846784.	
ACCESSION	AR064128	
VERSION	AR064128.1	GI:5993436
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 1364)	
AUTHORS	Hitz,W.D.	
TITLE	Fatty acid modifying enzymes from developing seeds of Vernonia	
JOURNAL	galanensis	
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Best Local Similarity		86.1%; Pred. No. 6.9e-200;
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Db	209	TAAAGAAAGCAATCCCTGCAATTCGTCGCGGATCCGCCGATTCGCCATCCGTTTCATCGTACG 268
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Db	269	TTGTTACAGGATCTCATTTATCACCTTCCTTTTATACAGCGTCGCCAACCTCTTACATTCCTC 328
Qy	300	ACCTCCCTCCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCAATCTTGCA 359
Db	329	TTCTCTCTCTCTCTCTACCTTACTTAGCATGCGGCTGTTTACTGGTTTGGCAATCTTGCA 388
Qy	360	TCCTCACTGGTTTATGGGTCTCGGCCATGAATCGGCCATCATGCTTATAGTAGTAC 419
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RESULT 4  
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LOCUS AX089471.1 1285 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 1 from Patent WO0116362.  
ACCESSION AX089471  
VERSION AX089471.1 GI:13443732  
KEYWORDS  
SOURCE  
ORGANISM  
Calendula officinalis  
Calendula officinalis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Asteroidae;  
Calenduleae; Calendula.  
1  
REFERENCE  
Feussner, I., Hornung, E., Fritsche, K., Peitzsch, N. and Renz, A.  
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Patent: WO 0116362-A 1 08-MAR-2001;  
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Best Local Similarity 77.2%; Pred. No. 4.1e-152;  
Matches 833; Conservative 0; Mismatches 140; Indels 6; Gaps 1;  
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RESULT 5  
AY166773 1419 bp mRNA linear PLN 02-JUN-2003  
LOCUS Helianthus annuus delta12-fatty acid acetylase mRNA, complete  
DEFINITION cds.  
ACCESSION AY166773  
VERSION AY166773.1 GI:31322134  
KEYWORDS Helianthus annuus (common sunflower)  
SOURCE Helianthus annuus  
ORGANISM Helianthus annuus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
REFERENCE 1 (bases 1 to 1419)  
AUTHORS Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.  
TITLE Fungal responsive fatty acid acetylases occur widely in  
evolutionarily distant plant families  
JOURNAL Plant J. 34 (5), 671-683 (2003)  
AUTHORS Cahoon, E.B.  
TITLE Direct Submission  
JOURNAL Submitted (18-OCT-2002) Crop Genetics, DuPont, Bldg. 402  
Experimental Station, Wilmington, DE 19880-0402, USA  
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Query Match 47.3%; Score 664.8; DB 4; Length 1419;  
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BD061165 1312 bp DNA linear PAT 27-AUG-2002  
LOCUS Plant fatty acid epoxigenase genes and uses therefor.  
DEFINITION BD061165  
ACCESSION BD061165.1 GI:22606771  
KEYWORDS JP 2001518797-A/2.  
SOURCE Crepis sp.  
ORGANISM Crepis sp.  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;



Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.

1 (bases 1 to 1312)

Stymne, S., Green, A., Singh, S. and Lenman, M.  
Plant fatty acid epoxigenase genes and uses therefor  
Patent: JP 2001518797-A 2 16-OCT-2001;  
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN  
STYMNE

COMMENT

OS Crepis sp.  
PN JP 2001518797-A/2  
PD 16-OCT-2001  
PR 09-APR-1998 JP 1998543302  
PR 15-APR-1997 AU PO 6223,15-APR-1997 AU PO 6226 PR  
16-APR-1997 US 60/043706,20-JUN-1997 US 60/050403 PI STEN  
STYMNE, ALLAN GREEN, SURINDER SINGH, MARIT LENMAN PC  
C12N15/53, C12N9/02  
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CC Topology: Linear;  
FH Key Location/Qualifiers  
FT CDS 26..1147.

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Query Match 46.8%; Score 657.6; DB 2; Length 1312;  
Best Local Similarity 76.4%; Pred. No. 2.2e-148;  
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AR367438 1312 bp mRNA linear PAT 12-SEP-2003

LOCUS Sequence 3 from patent US 6329518.

DEFINITION AR367438

ACCESSION AR367438.1 GI:34600637

VERSION

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1312)

AUTHORS Green, A., Singh, S., Lenman, M. and Stymne, S.

TITLE Plant fatty acid epoxigenase genes and uses therefor

JOURNAL Patent: US 6329518-A 3 11-DEC-2001;  
BASF Plant Science GmbH and Commonwealth Scientific & Industrial Research Organisation; Ludwigshafen;  
DEX;

FEATURES

source

1..1312 Location/Qualifiers  
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ORIGIN

Query Match 46.8%; Score 657.6; DB 2; Length 1312;  
Best Local Similarity 76.4%; Pred. No. 2.2e-148;  
Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGATTTGATCCGGCGCATTCCTGGTTCATCTCTAGTTCAGATCTCATT 196

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QY 197 GCACATTCCTCCGGGATCCGGCTCTGGTTCATCTCTAGTTCAGATCTCATT 256

DB 131 CCACATTCCTCCAGCGATGTCTATCGGTTCATCTTATTAGTGTTCAGATCTCATA 190

QY 257 ATCACCTTCCTTTTATACAGCGTCCGCAACACTACATTCCTCACTCCCTCCTCTCTA 316

DB 191 ATTGCTACATCTTCTACTCTCTGCAACATATATCCCTATCTCCCTCACTCTA 250

QY 317 GTTTACTTAGCATGCCGGTTTACTGTTTGGCAATCTTGCACTCTCACTGGTTTATGG 376

DB 251 GCCTACTTAGCTTGGCCGCTTACTGGTTCGTCAAGCTAGGCTCCTCACTGGGTATGG 310

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QY 557 CAGTCCGAGCTCAGACTTACTCCACATACGAAATTTCTTGACAAACCGCTGGTCGAATC 616

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QY 617 CTCATCTTGGTTCATCATGTGTAACCTTAGGATTCCTTTATACCTCTTAAACGAATGTTCA 676

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LOCUS AX031162 1312 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 3 from Patent W09846762.  
ACCESSION AX031162  
VERSION AX031162.1 GI:10278515

## KEYWORDS

## SOURCE

## ORGANISM

Crepis sp.

Crepis sp.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Crepis.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Green, A., Singh, S., Stymne, S. and Lenman, M.

Plant fatty acid epoxigenase genes and uses therefor

Patent: WO 9846762-A 3 22-OCT-1998;

GREEN ALLAN (AU); SINGH SURINDER (AU); COMMW SCIENT IND RES ORG

(AU); STYMNE STEN (SE); LENMAN MARIT (SE)

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Best Local Similarity

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76.4%; Pred. No. 2.2e-148;

836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

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QY 197 GCACATTCCTCCGGGATCCGGCTCTGGTCTCATCTCTAGTGTAGTTCAGGATCTCAAT 256

Db 131 CCACATTCCTCCGGGATCTGTCATTCCTTATACGTTGTTGAGGATCTCAT 190

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Db 1139 CATAAATGTGATC 1152

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LOCUS AY166777
DEFINITION Dimorphotheca sinuata delta12-fatty acid acetylase gene, partial cds.
ACCESSION AY166777
VERSION AY166777.1 GI:31322142
KEYWORDS Dimorphotheca sinuata (African daisy)
SOURCE Dimorphotheca sinuata
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroidae;
Calenduleae; Dimorphotheca.
REFERENCE 1 (bases 1 to 979)
AUTHORS Cahoon,E.B., Schurr,J.A., Huffman,E.A. and Minto,R.E.
TITLE Fungal responsive fatty acid acetylases occur widely in
evolutionarily distant plant families
JOURNAL Plant J. 34 (5), 671-683 (2003)
REFERENCE 2 (bases 1 to 979)
AUTHORS Cahoon,E.B.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Crop Genetics, DuPont, Bldg. 402
Experimental Station, Wilmington, DE 19880-0402, USA
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DEFINITION	Plant fatty acid epoxigenase genes and uses therefor.		
ACCESSION	BD061164		
VERSION	BD061164.1	GI:22606770	
KEYWORDS	JP 2001518797-A/1.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Stymne, S., Green, A., Singh, S. and Lemman, M.		
TITLE	Plant fatty acid epoxigenase genes and uses therefor		
JOURNAL	Patent: JP 2001518797-A 1 16-OCT-2001; COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN STYMNE		
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QY	1157	AAGGAATGCAITTTATCATCGAGCAAGATCGACAGACACAAAGGAGACATATTTGGTAC	1216		
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DEFINITION	CS023951				PAT 03-MAR-2005
ACCESSION	CS023951				
VERSION	CS023951.1	GI:60495634			
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ORGANISM	Crepis palaeolina				
REFERENCE					
AUTHORS	Poirier, Y., Rezzonico, E. and Moire, L.				
TITLE	Fatty acid biosynthesis 1				
JOURNAL	Patent: WO 2005014833-A 3 17-FEB-2005;				
	The University of York (GB)				
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ACCESSION AR367437
VERSION AR367437.1 GI:34600636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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VERSION AX031160.1 GI:10278513
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 unclassified sequences.
AUTHORS Green,A., Singh,S., Stymne,S. and Lenman,M.
TITLE Plant fatty acid epoxigenase genes and uses therefor
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ORIGIN
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